

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 13:48:23 ; Search time 156 Seconds  
(without alignments)  
427.716 Million cell updates/sec

Title: US-10-650-417-7

Perfect score: 978

Sequence: 1 VGLNLCIVAVSQNMIGIKNG.....SDVQEKGIKYKFEVVEKND 186

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	186	8	ADK19667 Human di
2	968	99.0	186	3	AAY63976 DHFR-HM p
3	968	99.0	187	4	AAM33902 Human pol
4	968	99.0	187	8	ADQ09318 Human DHF
5	957.5	97.9	187	2	AAW81770 DHFR-HM p
6	880	90.0	186	6	ABR56964 Mouse di
7	880	90.0	186	7	ADD45852 Rat Prote
8	880	90.0	187	2	AAW37340 Mouse di
9	880	90.0	187	7	ADK60366 Rat Frote
10	878	89.8	187	8	ADK19665 Rat dihyd
11	875	89.5	187	8	ADN99572 Novel hum
12	875	89.5	187	8	ADN99573 Novel hum
13	874	89.4	186	1	AAP40064 Sequence
14	874	89.4	198	4	AAM41688 Human pol
15	874	89.4	204	2	AAW07470 Transcrip
16	874	89.4	209	2	AAW07471 Transcrip
17	874	89.4	266	1	AAP91236
18	874	89.4	524	2	AAW98136 (Hexahis)
19	874	89.4	539	2	AAW98137 DHFR/HPH
20	874	89.4	539	2	AAW98138 DHFR/HPH
21	869	88.9	186	2	AAW05742 376-2400
22	866	88.5	471	2	AAW27246 Sequence
23	864	88.3	193	2	AAW78376 Heat-indu
24	864	88.3	193	2	AAW99400 N-termina
25	864	88.3	297	4	AAB61618 MGP-DHFR

26	864	88.3	368	3	AAB12253
27	864	88.3	439	3	AAB12252
28	862	88.1	187	8	ADK19666
29	844.5	86.3	218	4	ABG16781 Novel hum
30	792.5	81.0	203	4	AAU30726 Novel hum
31	729	74.5	141	6	ABR56985
32	658	67.3	141	6	ABR56986
33	599.5	61.3	188	3	AAB53124
34	587.5	60.1	188	8	ADK19664
35	553	56.5	141	6	ABR56967
36	472.5	48.3	210	2	AAW40101
37	472.5	48.3	210	2	AAW82437
38	393	40.8	182	4	ABR69904
39	295.5	30.2	206	2	AAK12277
40	293.5	30.0	206	2	AAK28837
41	284	29.0	612	2	AAU17271
42	239	24.4	168	4	AAU36186
43	239	24.4	168	6	ABU38240
44	239	24.4	168	8	ADQ25537
45	239	24.4	168	8	ADQ25539

#### ALIGNMENTS

RESULT 1

ADK19667

ID ADK19667 standard; protein; 186 AA.

XX AC ADK19667;

XX DT 03-JUN-2004 (first entry)

XX DE Human dihydrofolate reductase (DHFR) polypeptide.

XX KW Human; dihydrofolate reductase; DHFR; methotrexate; herpes simplex virus;

XX KW thymidine kinase; cytosine deaminase; pro-apoptotic gene;

XX KW immunostimulatory molecule; tumour suppressor gene; beta-globin protein;

XX KW green fluorescent protein; cancer; colorectal; liver; pancreas; lymphoma;

XX KW lung; prostate; breast; suicide gene; cyrostatic; enzyme.

XX OS Homo sapiens.

XX PN US2004053836-A1.

XX PD 18-MAR-2004.

XX PF 22-APR-2003; 2003US-00421285.

XX PR 22-APR-2002; 2002US-0375250P.

XX PA (MAYE/) MAYER-KUCKUK P.

XX PA (BANE/) BANERJEE D.

XX PA (BERT/) BERTINO J.

XX PI Mayer-Kuckuk P, Banerjee D, Bertino J;

XX DR WPI; 2004-247775/23.

XX PT Novel cDNA molecule encoding fusion protein that comprises mammalian

XX PT dihydrofolate reductase and a therapeutic protein such as product of

XX PT tumor suppressor gene, useful for treating colorectal cancer, liver

XX PT cancer, pancreatic cancer.

XX PS Disclosure; SEQ ID NO 5; 27pp; English.

XX CC The invention relates to a cDNA molecule encoding a fusion protein that

XX CC comprises a mammalian dihydrofolate reductase (DHFR) and a therapeutic

XX CC protein. The fusion protein comprises a wild-type mammalian DHFR such as

XX CC rat, mouse, dog, monkey or human DHFR. Optionally, the fusion protein

XX CC comprises a mutant form of DHFR, preferably a mutant form of human DHFR,

XX CC where the mutant form has increased resistance to methotrexate. The cDNA

XX CC molecule is useful for providing enhanced delivery of a therapeutic

CC protein to a mammalian subject which involves administering the cDNA. The  
 CC therapeutic protein is a protein that enhances toxicity of an  
 CC administered drug such as a mutant or wild-type form of herpes simplex  
 CC virus thymidine kinase or cytosine deaminase. The therapeutic protein is  
 CC a product of a pro-apoptotic gene, an immunostimulatory molecule, a  
 CC product of a tumor suppressor gene or a functional protein useful in  
 CC gene therapy such as a wild-type or enhanced beta-globin protein. The  
 CC cDNA further comprises a region encoding a reporter protein such as green  
 CC fluorescent protein. The cDNA molecules can be used for treating a wide  
 CC variety of cancer cells e.g., colorectal cancer, liver cancer, pancreatic  
 CC cancer, lymphomas, lung cancer, prostate cancer and breast cancer using  
 CC suicide genes as therapeutic genes. This sequence represents a human DHFR  
 CC polypeptide of the invention.

XX Sequence 186 AA;

Query Match 100.0%; Score 978; DB 8; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-99;  
 Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VGSNCIVAVSQNMGIGKNGDLPWFLNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60  
 DB 1 VGSNCIVAVSQNMGIGKNGDLPWFLNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60  
 QY 61 PEKNRPLKGRINLVLSRELKEPPQCAHFLSRSLDDALKLTQPELANKVDVWVVGSSV 120  
 DB 61 PEKNRPLKGRINLVLSRELKEPPQCAHFLSRSLDDALKLTQPELANKVDVWVVGSSV 120  
 QY 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLLPEYPGVLSVQBEKGKIKYKFE 180  
 DB 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLLPEYPGVLSVQBEKGKIKYKFE 180  
 QY 181 VYEKND 186  
 DB 181 VYEKND 186

RESULT 2

AAY69976  
 ID AAY69976 standard; protein; 186 AA.

XX AAY69976;  
 AC AAY69976;

DT 13-APR-2000 (first entry)

DE DHFR-HM protein.

Protein sequence database; biological function determination;  
 enzymatic activity; signaling activity; protein function determination;  
 DHFR-HM.

OS Homo sapiens.

PN WO9962004-A1.

XX 02-DEC-1999.

PF 26-MAY-1998; 98WO-JP002302.

PR 26-MAY-1998; 98WO-JP002302.

XX (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.

XX Itai A, Tomioka N, Itai R, Imamura M;

XX WPI; 2000-136797/12.

XX An efficient, accurate and rapid computer database for estimating protein  
 XX functions e.g. enzymatic activity, for polypeptides obtained from gene  
 XX sequence translation.

XX Example 2; Fig 2; 26pp; Japanese.

CC This sequence represents the human DHFR protein. The invention relates to  
 CC a database containing information on the amino acid (aa) sequences of  
 CC proteins of which 1 or more biological functions are known. The database  
 CC also contains additional information on the score of importance of each  
 CC aa residue in the whole aa sequence in determining the known biological  
 CC functions. The invention also relates to a method of preparing an  
 CC alignment between aa sequences contained in the database and those of the  
 CC unknown polypeptide. This is represented as the homology amongst various  
 CC sites, each being identified as having a high score of importance in  
 CC determining potential biological functions. The method is used to enable  
 CC an efficient estimation of the biological functions (particularly  
 CC enzymatic and signaling activities) of polypeptides from their aa  
 CC sequences. Suitable proteins can then be isolated and purified by various  
 CC means. This could be of considerable use in a biological and medical  
 CC context. The computerised procedure is efficient, fast and accurate

XX Sequence 186 AA;

Query Match 99.0%; Score 968; DB 3; Length 186;  
 Best Local Similarity 99.5%; Pred. No. 1.1e-97;  
 Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VGSNCIVAVSQNMGIGKNGDLPWFLNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60  
 DB 1 VGSNCIVAVSQNMGIGKNGDLPWFLNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60  
 QY 61 PEKNRPLKGRINLVLSRELKEPPQCAHFLSRSLDDALKLTQPELANKVDVWVVGSSV 120  
 DB 61 PEKNRPLKGRINLVLSRELKEPPQCAHFLSRSLDDALKLTQPELANKVDVWVVGSSV 120  
 QY 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLLPEYPGVLSVQBEKGKIKYKFE 180  
 DB 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLLPEYPGVLSVQBEKGKIKYKFE 180  
 QY 181 VYEKND 186  
 DB 181 VYEKND 186

RESULT 3

AAM39902  
 ID AAM39902 standard; protein; 187 AA.

XX AAM39902;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 3047.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 XX peripheral nervous system; neuropathy; central nervous system; CNS;  
 XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 XX leukaemia.

OS Homo sapiens.

PN WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.



Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVINGKKTWFSI 60  
DB 2 VGSNCIVAVSQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVINGKKTWFSI 61  
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 120  
DB 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 121  
QY 121 YKEAMNHPGHLKLVTRIMQDFSDTFPEIDLEKYKLLPEYGVLSVQVEKGIKYKF 180  
DB 122 YKEAMNHPGHLKLVTRIMQDFSDTFPEIDLEKYKLLPEYGVLSVQVEKGIKYKF 181  
QY 181 VYEKND 186  
DB 182 VYEKND 187

## RESULT 5

AAW81770 standard; peptide; 187 AA.

AC AAW81770;

DT 17-OCT-2003 (revised)

ET 29-JAN-1999 (first entry)

XX DIHR-HM peptide fragment.

XX DIHR; dihydrofolic acid reductase; protein function; trypsin;

XX ribonuclease; myoglobin; database; homology; resemblance.

XX unidentified.

XX JPI0287696-A.

XX 27-OCT-1998.

XX 11-APR-1997; 97JP-00093577.

XX 11-APR-1997; 97JP-00093577.

XX (YAK-) IYAKU BUNSHI SEKKEI KENKYUSHO KK.

XX WPI; 1998-018384/02.

XX Determination of protein biological function - comprises use of amino

XX acid sequences database containing the relevant information.

XX Example 2; Fig 2; 11pp; Japanese.

XX This sequence is used in the creation of a database containing the

XX information for amino acid sequence of protein with at least 1 biological

XX function with added a score on importance of expression of the biological

XX information for each amino acid residue. The database is useful for

XX determination of unknown biological function of a protein or polypeptide

XX based on the homology of amino acid sequence, e.g. steric structure of

XX protein, and includes retrieval and evaluation of high homologous

XX relationship for the determination of mostly resembling protein. The

XX database allows for correct and rapid retrieval and presumption of

XX protein and polypeptide having biological functions. (Updated on 17-OCT-

XX 2003 to standardise OS field)

XX Sequence 187 AA;

Query Match

Best Local Similarity 97.9%; Score 957.5; DB 2; Length 187;

Matches 185; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 VGSNCIVAVSQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVINGKKTWFSI 60

DB 1 VGSNCIVAVSQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVINGKKTWFSI 60

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 119  
DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 120  
QY 120 VYKEAMNHPGHLKLVTRIMQDFSDTFPEIDLEKYKLLPEYGVLSVQVEKGIKYKF 179  
DB 121 VYKEAMNHPGHLKLVTRIMQDFSDTFPEIDLEKYKLLPEYGVLSVQVEKGIKYKF 180  
QY 180 VYEKND 186  
DB 181 VYEKND 187

## RESULT 6

ABR56964 standard; protein; 186 AA.

AC ABR56964;

DT 04-AUG-2003 (first entry)

DE Mouse dihydrofolate reductase amino acid sequence #1.

XX Dihydrofolate reductase; DYR; enzyme; browser; genetic; gene; database.

XX Mus musculus.

XX NC02003017138-A1.

XX 27-FEB-2003.

XX 20-AUG-2002; 2002WO-JP008368.

XX 21-AUG-2001; 2001US-0313488P.

XX (MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.

XX Fukuda M, Shigetaka M, Tomioka N, Itai A;

XX WPI; 2003-268379/26.

XX Method of browsing genetic sequences comprises specifying sequences,

XX determining similarity against database records, and displaying similar

XX sequences from database together with specified sequences.

XX Example 1; Fig 2; 39pp; Japanese.

XX The present invention describes a method for browsing genetic sequences.

XX The method comprises: (a) specifying one or more sequences to view; (b)

XX determining the similarities of the sequence to be viewed against the

XX records in the users database; and (c) when there are similarities, the

XX records from the database and the sequence to be viewed are displayed

XX together. The method can be used for browsing gene sequences. The

XX information retrieved is stored in the user side database, and therefore

XX the information is easy to read. The present sequence represents a mouse

XX dihydrofolate reductase (DYR) amino acid sequence, which is used in the

XX exemplification of the present invention

XX Sequence 186 AA;

Query Match

Best Local Similarity 90.0%; Score 880; DB 6; Length 186;

Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVINGKKTWFSI 60

DB 1 VPLNCIVAVSQNMIGKNGDLPPFLRNEFKYFQMTTSSVEGKQNLVINGKKTWFSI 60

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 120

DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWIVGSSV 120

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CC  ftp.wipo.int/pub/published_pct_sequences.
XX
SQ  Sequence 186 AA;

Query Match          90.0%; Score 880; DB 7; Length 186;
Best Local Similarity 89.2%; Pred. No. 5.1e-88;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0

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**Qy**

1 VGSINCIIVASQNMGIGKNGDLPPPLRNEFRYFORMTTTSSVEGKNLVINGKKTWFSI 60  
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| | | | | : | | | | | : | | | | |

**Dd**

1 VRPLNCIIVASQNMGIGKNGDLPPPLRNEFKYFORMTTTSSVEGKNLVINGRKTWFSI 60  
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QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMMWVGSSV 1200

Db 61 PEKNRPLKDRINIVLSRELKEPPRGAHFLAKSLDDALRLIEQPELASKVDMVWIVGSSV 120

QY 121 YKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGLSDVQEEKGIKYKFE 180

QV	181	VVEKND	186
Db	121	QYENKQPGHLURLFVTRIMQEFESDTFFPEIDLKGYKLLPEIPGVLSVQEEKGIKKFE	180

191 WFAZ 196

## RESULT 8

ID AAW37340 standard; protein; 187 AA.

AC AAW37340;

DT 11-MAY-1998 (first entry)

DE Mouse dihydrofolate reductase.

XX  
KW  
Vaccine: B-cell malignancy: lymphoma: leukaemia: tumour:

KW gene amplification; immunotherapy; therapy; mouse; DHFR;  
KW dihydrofolate reductase; vector; rccm7 puen

XX C M.C. 100.7.18

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XX PD 06-NOV-1997-

XX  
PF 25-APR-1997. 97W0-IIS007039

XX  
PR 01-MAY-1996; 96US-00644654.  
PR 06-DEC-1996; 96US-00761277.  
XX

(GENI-) GENITOPE CORP.  
Denney DW;  
WPI: 1997-549743/50.  
N-PSDB; AAT97170.  
Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at least 2 different recombinant variable regions of immunoglobulin molecules derived from B cell lymphoma cells.  
Example 3; Page 111; 177pp; English.  
This protein comprises mouse dihydrofolate reductase (DHFR). The DHFR coding sequence (see AAT97170) was utilised in the construction of an amplification vector pSSD75-DHFR, which contains the DHFR cDNA under control of the SV40 enhancer/promoter. The vector allows the selection of cell lines which have amplified the vector sequences by selecting for cells able to grow in increasing concentrations of methotrexate. The invention provides vectors and improved methods for the expression and co-amplification of genes encoding recombinant proteins in cultured cells. The methods permit the isolation of cell lines which have co-amplified invariant recombinant sequences which encode an amplifiable marker gene ex

CC more expression vectors encoding a protein of interest and optionally a  
 CC selectable marker. The amplified cells provide large quantities of  
 CC recombinant proteins suitable for immunotherapy for treatment of  
 CC lymphomas and leukaemias. The methods permit the production of custom  
 CC vaccines, including multivalent vaccines, that reflect the degree of  
 CC somatic variation found in a patient's tumour

XX Sequence 187 AA;

CC Query Match 90.0%; Score 880; DB 2; Length 187;  
 CC Best Local Similarity 89.2%; Pred. No. 5.2e-88;  
 CC Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;  
 CC  
 CC 1 VGSNCIVAVSQNMIGKNGDLPWFLNRPYFQRMFTTSSVEGKQNLVIMGKKTWFSI 60  
 CC 2 VRPLNCIVAVSQNMIGKNGDLPWFLNRPYFQRMFTTSSVEGKQNLVIMGKKTWFSI 61  
 CC  
 CC 61 PEKNRPLKGRINVLVSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMWIVGSSV 120  
 CC 62 PEKNRPLKDRINIVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMWIVGSSV 121  
 CC  
 CC 121 YKEAMNHGHLKLFVTRIMQFESDTFFPEIDLEKYKLLPEYPGVLSVQVEEKGIKYKFE 180  
 CC 122 YQEMNQPGHLRLFVTRIMQFESDTFFPEIDLEKYKLLPEYPGVLSVQVEEKGIKYKFE 181  
 CC  
 CC 181 VYEKND 186  
 CC 182 VYEKND 187

# RESULT 9

AD 60366 standard; protein; 187 AA.

AC ADE60366;

DE 29-JAN-2004 (first entry)

DE Rat Protein AAH05796, SEQ ID NO 6273.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX {GEHO } GEN HOSPITAL CORP.

XX {FARB } BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX MPI; 2003-268312/26.

XX GENBANK; AAH05796.

XX New composition comprising two or more isolated polypeptides, useful for  
 XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC the sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 187 AA;

CC Query Match 90.0%; Score 880; DB 7; Length 187;

CC Best Local Similarity 89.2%; Pred. No. 5.2e-88;

CC Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

CC 1 VGSNCIVAVSQNMIGKNGDLPWFLNRPYFQRMFTTSSVEGKQNLVIMGKKTWFSI 60  
 CC 2 VRPLNCIVAVSQNMIGKNGDLPWFLNRPYFQRMFTTSSVEGKQNLVIMGKKTWFSI 61  
 CC  
 CC 61 PEKNRPLKGRINVLVSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMWIVGSSV 120  
 CC 62 PEKNRPLKDRINIVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMWIVGSSV 121  
 CC  
 CC 121 YKEAMNHGHLKLFVTRIMQFESDTFFPEIDLEKYKLLPEYPGVLSVQVEEKGIKYKFE 180  
 CC 122 YQEMNQPGHLRLFVTRIMQFESDTFFPEIDLEKYKLLPEYPGVLSVQVEEKGIKYKFE 181  
 CC  
 CC 181 VYEKND 186  
 CC 182 VYEKND 187

# RESULT 10

ADK19665

ID ADK19665 standard; protein; 187 AA.

XX ADK19665;

XX 03-JUN-2004 (first entry)

DE Rat dihydrofolate reductase (DHFR) polypeptide.

XX Rat; dihydrofolate reductase; DHFR; methotrexate; herpes simplex virus;  
 KW thymidine kinase; cytosine deaminase; pro-apoptotic gene;  
 KW immunostimulatory molecule; tumour suppressor gene; beta-globin protein;  
 KW green fluorescent protein; cancer; colorectal; liver; pancreas; lymphoma;  
 KW lung; prostate; breast; suicide gene; cytostatic; enzyme.

XX Rattus sp.

XX US2004053836-A1.

XX 18-MAR-2004.

XX 22-APR-2003; 2003US-00421285.

XX 22-APR-2002; 2002US-0375250P.

XX (MAYE/) MAYER-KUCKUK P.



PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
 PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;  
 PI Wong JGP, Wu G, Zhang H, Zeng C;  
 XX WPI; 2004-365511/34.  
 DR N-PSDB; ADN98789.

XX New nucleic acid molecules, useful in preparing a composition for  
 PT treating or preventing e.g. inflammatory, CNS, bacterial or viral  
 PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or  
 PT ulcerative colitis.

XX Claim 14; SEQ ID NO 1172; 532pp; English.

XX The invention relates to a nucleic acid molecule comprising a  
 CC polynucleotide sequence or its complement that encodes a polypeptide. The  
 CC nucleic acid is useful in preparing a composition for treating or  
 CC preventing inflammatory, CNS, immune, bacterial or viral disorder.  
 CC Cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic  
 CC heart disease or ulcerative colitis. This sequence corresponds to a  
 CC protein of the invention.

XX Sequence 187 AA;

Query Match 89.5%; Score 875; DB 8; Length 187;

Best Local Similarity 92.9%; Pred. No. 1,8e-87;

Matches 170; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

4 LNCIVAVSQMGIKNGNDLPWPLNRPYFQMTTSSVEGKQNLVINGKKTWFSIPEX 63

5 LNCIVAVSQMGIKNGNDLPWPLNRPYFQMTTSSVEGKQNLVINGKKTWFSIPEX 64

64 NRPLKGRINLVLSRELKPEPQGAHFLSRSLDALKLTERPELANKVDWIVGGSSVYKE 123

65 NRPLKGRINLVLSRELKPEPQGAHFLSRSLDALKLTERPELANKVDWIVGGSSVYKE 124

124 AMNHGHLKLVTRIMQDPESDTFFSIDLEKYLLEPYGVLSDVQEEKIKYKFEVYE 183

125 AMNHGHLKLVTRIMQDPESDTFFSIDLEKYLLEPYGVLSDVQEEKIKYKFEVCE 184

184 KND 186

185 KOD 187

RESULT 12

ADN99573

ID ADN99573 standard; protein; 187 AA.

AC ADN99573;

XX 29-JUL-2004 (first entry)

XX Novel human protein sequence #389.

XX anti-inflammatory; dermatological; neuroprotective; immunomodulator;  
 KM antibacterial; virucide; antipsoriatic; cytostatic; gene therapy;  
 KM vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes;  
 KM early aging; hormonal imbalance; ischemic heart disease;  
 KM ulcerative colitis.

XX Homo sapiens.

XX WO2004038003-A2.

XX 06-MAY-2004.

XX 24-OCT-2003; 2003WO-US033947.

XX 25-OCT-2002; 2002US-0421061P.

XX 25-OCT-2002; 2002US-0421080P.

PR 25-OCT-2002; 2002US-0421552P.  
 PR 25-OCT-2002; 2002US-0421614P.  
 PR 30-OCT-2002; 2002US-0422177P.  
 PR 30-OCT-2002; 2002US-0422178P.  
 PR 15-NOV-2002; 2002US-0426355P.  
 PR 15-NOV-2002; 2002US-0426384P.  
 PR 15-NOV-2002; 2002US-0426394P.  
 PR 15-NOV-2002; 2002US-0426430P.  
 PR 15-NOV-2002; 2002US-0426916P.  
 PR 27-NOV-2002; 2002US-0429275P.  
 PR 27-NOV-2002; 2002US-0429275P.  
 PR 27-NOV-2002; 2002US-0429302P.  
 PR 27-NOV-2002; 2002US-0429328P.  
 PR 27-NOV-2002; 2002US-0429651P.  
 PR 04-DEC-2002; 2002US-0430645P.  
 PR 04-DEC-2002; 2002US-0430651P.  
 PR 04-DEC-2002; 2002US-0430657P.  
 PR 04-DEC-2002; 2002US-0430663P.  
 PR 04-DEC-2002; 2002US-0430668P.  
 PR 04-DEC-2002; 2002US-0430684P.  
 PR 05-DEC-2002; 2002US-0430937P.  
 PR 05-DEC-2002; 2002US-0430965P.  
 PR 05-DEC-2002; 2002US-0431458P.  
 PR 12-DEC-2002; 2002US-0433251P.  
 PR 12-DEC-2002; 2002US-0433500P.  
 PR 13-DEC-2002; 2002US-0433316P.  
 PR 13-DEC-2002; 2002US-0433318P.  
 PR 23-DEC-2002; 2002US-0436236P.  
 PR 03-JAN-2003; 2003US-0437914P.  
 PR 17-JAN-2003; 2003US-0440820P.  
 PR 18-APR-2003; 2003US-0440821P.  
 PR 18-APR-2003; 2003US-0463700P.  
 PR 18-APR-2003; 2003US-0463708P.  
 PR 18-APR-2003; 2003US-0463716P.  
 PR 18-APR-2003; 2003US-0463732P.  
 PR 02-MAY-2003; 2003US-0467139P.  
 PR 02-MAY-2003; 2003US-0467201P.  
 PR 02-MAY-2003; 2003US-0467203P.  
 PR 02-MAY-2003; 2003US-0467230P.  
 PR 19-MAY-2003; 2003US-0471306P.  
 PR 19-MAY-2003; 2003US-0471336P.  
 PR 22-MAY-2003; 2003US-0472420P.  
 PR 22-MAY-2003; 2003US-0472430P.  
 PR 09-JUN-2003; 2003US-0476609P.  
 PR 09-JUN-2003; 2003US-0476621P.  
 PR 09-JUN-2003; 2003US-0476632P.  
 PR 08-JUL-2003; 2003US-0476641P.  
 PR 08-JUL-2003; 2003US-0485217P.  
 PR 08-JUL-2003; 2003US-0485218P.  
 PR 08-JUL-2003; 2003US-0485223P.  
 PR 08-JUL-2003; 2003US-0485224P.  
 PR 08-JUL-2003; 2003US-0485325P.  
 PR 08-JUL-2003; 2003US-0485359P.  
 PR 14-JUL-2003; 2003US-0486446P.  
 PR 14-JUL-2003; 2003US-0486480P.  
 PR 15-JUL-2003; 2003US-0486891P.  
 PR 15-JUL-2003; 2003US-0486960P.  
 PR 08-AUG-2003; 2003US-0493341P.  
 PR 08-AUG-2003; 2003US-0493370P.  
 PR 08-AUG-2003; 2003US-0493573P.  
 PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
 PI Halenbeck RF, Kothakota S, Lin H, Linnemann T, Pierce K, Wang Y;  
 PI Wong JGP, Wu G, Zhang H, Zeng C;

XX WPI; 2004-365511/34.

XX N-PSDB; ADN98789.

XX New nucleic acid molecules, useful in preparing a composition for  
 PT treating or preventing e.g. inflammatory, CNS, bacterial or viral



PT disorders, cancer, psoriasis, diabetes, ischemic heart disease or  
XX ulcerative colitis.

PS Claim 14; SEQ ID NO 1173; 532pp; English.

XX The invention relates to a nucleic acid molecule comprising a  
CC polynucleotide sequence or its complement that encodes a polypeptide. The  
CC nucleic acid is useful in preparing a composition for treating or  
CC preventing inflammatory, CNS, immune, bacterial or viral disorder,  
CC cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic  
CC heart disease or ulcerative colitis. This sequence corresponds to a  
XX protein of the invention.

SQ Sequence 187 AA;

Query Match 89.5%; Score 875; DB 8; Length 187;  
Best Local Similarity 92.9%; Pred. No. 1.8e-87;  
Matches 170; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
QY 4 LNCIVAVSQNMIGKNGDLPWFLRNEFRYFQRMFTTSSVEGKQNLVINGKKTWFSIPEK 63  
DB 5 LNCIVAVSQNMIGKNGDLPWFLRNEFRYFQRMFTTSSVEGKQNLVINGKKTWFSIPEK 64  
QY 64 NRPLKGRINLVLSRELKEPPQGAHFLSRLDDALKLTPQELANKVDWVIWVGSSVYKE 123  
DB 65 NRPLKGRINLVLSRELKEPPQGAHFLSRLDDALKLTPQELANKVDWVIWVGSSVYKE 124  
QY 124 ANNHGHLKLVFTRIMQDFSDTFFPEIDLEKYLPEYGVLSDVQBEKGKIKYKFEVYE 183  
DB 125 ANNHGHLKLVFTRIMQDFSDTFFPEIDLEKYLPEYGVLSDVQBEKGKIKYKFEVCE 184  
QY 184 KND 186  
DB 185 KDD 187

RESULT 13

AAP40064  
ID AAP40064 standard; protein; 186 AA.

XX  
AC AAP40064;

XX 09-JAN-1992 (first entry)

XX Sequence of dihydrofolate reductase (DHFR 3T6-R400), a DHFR enzyme  
DE produced by a mutant line of mouse fibroblast cells.

XX Genetic marker; drug resistance; decreased methotrexate affinity.

XX Mus musculus.

XX Key Location/Qualifiers

FT Misc-difference 22 /note= "Leu in wt. DHFR"

XX  
PN EP117060-A.

XX 29-AUG-1984.

XX 18-JAN-1984; 84EP-00300300.

XX 19-JAN-1983; 83US-00459151.

XX (GETH ) GENENTECH INC.

XX Levinson AD, Simonsen CC, Yelverton EM;

XX WPI; 1984-214789/35.

XX N-PSDB; AAN40061.

XX Plasmid with DNA coding for dihydro-folate reductase protein - opt. with  
PT sequence encoding heterologous protein operatively linked.

XX

PS Disclosure; Fig 1b; 52pp; English.

XX DHFR 3T6-R400 has a low binding affinity for methotrexate (MTX) a known  
CC inhibitor of DHFR. The present invention thus enables growth of wild type  
CC cells transformed with sequences coding for the modified DHFR at MTX  
CC concentrations which would ordinarily be lethal. It permits detection of  
CC cells that have been transformed with a vector, also including the coding  
CC sequence for a desired heterologous protein

SQ Sequence 186 AA;

Query Match 89.4%; Score 874; DB 1; Length 186;  
Best Local Similarity 88.7%; Pred. No. 2.3e-87;  
Matches 165; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 VSLNCIVAVSQNMIGKNGDLPWFLRNEFRYFQRMFTTSSVEGKQNLVINGKKTWFSI 60  
DB 1 VRPLNCIVAVSQNMIGKNGDLPWFLRNEFRYFQRMFTTSSVEGKQNLVINGKKTWFSI 60  
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRLDDALKLTPQELANKVDWVIWVGSSV 120  
DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRLDDALKLTPQELANKVDWVIWVGSSV 120  
QY 121 YKEAMNHGHLKLVFTRIMQDFSDTFFPEIDLEKYLPEYGVLSDVQBEKGKIKYKFE 180  
DB 121 YQEAAMNQGHLLFVTRIMQBEFSDTFFPEIDLGKYLPEYGVLSVQBEKGKIKYKFE 180  
QY 181 VYKND 186  
DB 181 VYKND 186

RESULT 14

AAM41688  
ID AAM41688 standard; protein; 198 AA.

XX  
AC AAM41688;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6619.

XX Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-004711275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-0052317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00820312.

XX 03-AUG-2000; 2000US-00853450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AU, Yang Y, Zhang J, Zhao QA;

XX Zhou P, Goodrich R, Drmanac RT;

DR WPI; 2001-442253/47.  
 DR N-PSDB; AA160844.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders such  
 PT as central nervous system injuries.  
 XX  
 PS Example 2; SEQ ID NO 6619; 10078pp; English.  
 XX  
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the  
 CC encoded polypeptides (AA157798-AA161369) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilization of the activities such as: Immune system suppression,  
 CC Aggravation/inhibition activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification  
 XX  
 SQ Sequence 198 AA;  
 Query Match 89.4%; Score 874; DB 4; Length 198;  
 Best Local Similarity 92.3%; Pred. No. 2.6e-87;  
 Matches 169; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 4 LNCIVAVSQNMIGKNGDLPWPFLENEFRYFQRMVTTSSVEGKQNLVIMGKKTWFSIPEX 63  
 DB 16 LNCIVAVSQNMIGKNGDLPWPFLENEFRYFQRMVTTSSVEGKQNLVIMGKKTWFSIPEX 75  
 QY 64 NRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMWIVGSSVYKE 123  
 DB 76 NRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMWIVGSSVYKE 135  
 QY 124 AMNHGHLKLVTRIMQDFESDTPFPIDLEKYKLLPEYPGVLSDVQEGKIKYKFEVE 183  
 DB 136 AMNHGHLKLVTRIMQDFESDTPFPIDLEKYKLLPEYPGVLSDVQEGKIKYKFEVE 195  
 QY 184 KND 186  
 DB 196 KDD 198  
 RESULT 15  
 AAR07470  
 ID AAR07470 standard; protein; 204 AA.  
 AC AAR07470;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 29-JAN-1991 (first entry)  
 XX  
 XX Transcript of plasmid pDS781/RBSII, 6xHis under the control of RBSII.  
 XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;  
 XX hypersensitivity.  
 XX Homo sapiens.  
 XX  
 XX EP393502-A.  
 XX  
 XX 24-OCT-1990.  
 XX  
 XX 11-APR-1990; 90EP-00106992.  
 XX  
 XX 19-APR-1989; 89EP-00810295.  
 XX  
 XX (HOFF) HOFFMANN-LA ROCHE AG.  
 XX

PI Fountoulak M, Garotta G, Stuber D;  
 XX WPI; 1990-322042/43.  
 DR N-PSDB; AAQ06305.  
 XX  
 PT Soluble interferon-gamma receptors - for treating auto-immune diseases,  
 PT chronic inflammations, etc.  
 XX  
 PS Disclosure; Fig 12; 174pp; English.  
 XX  
 CC IFN-gamma is a therapeutically active agent in the treatment of  
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,  
 CC chronic inflammations and delayed hypersensitivity. It is also useful in  
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 204 AA;  
 Query Match 89.4%; Score 874; DB 2; Length 204;  
 Best Local Similarity 89.7%; Pred. No. 2.7e-87;  
 Matches 165; Conservative 12; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 VGSNCIVAVSQNMIGKNGDLPWPFLENEFRYFQRMVTTSSVEGKQNLVIMGKKTWFSI 60  
 DB 16 VRELNCIVAVSQNMIGKNGDLPWPFLENEFRYFQRMVTTSSVEGKQNLVIMGKKTWFSI 75  
 QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMWIVGSSV 120  
 DB 76 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTPQELANKVDMWIVGSSV 135  
 QY 121 YEAMNHGHLKLVTRIMQDFESDTPFPIDLEKYKLLPEYPGVLSDVQEGKIKYKFE 180  
 DB 136 YQEAAMNHGHLKLVTRIMQDFESDTPFPIDLEKYKLLPEYPGVLSDVQEGKIKYKFE 195  
 QY 181 VYEK 184  
 DB 196 VYEK 199  
 Search completed: November 19, 2004, 13:52:23  
 Job time : 160 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 13:48:23 ; Search time 39 Seconds  
(without alignments)  
316.286 Million cell updates/sec

Title: US-10-650-417-7

Perfect score: 978  
Sequence: 1 VGLNCIVAVSQNMIGKNG.....SDVOEKGIGYKFEVYEKND 186

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pap: \*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pap: \*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pap: \*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pap: \*  
5: /cgn2\_6/prodata/1/iaa/6C COMB.pap: \*  
6: /cgn2\_6/prodata/1/iaa/6D COMB.pap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	978	100.0	186	4	US-09-142-530C-7
2	956	97.8	186	3	US-09-230-637-36
3	892	91.2	187	3	US-09-347-878-28
4	880	90.0	187	1	US-08-644-6648-19
5	880	90.0	187	2	US-08-761-277A-19
6	880	90.0	187	5	PCI-US94-00658-3
7	874	89.4	471	1	US-08-257-341-9
8	874	89.4	524	3	US-08-557-210A-3
9	874	89.4	539	3	US-08-557-210A-4
10	874	89.4	539	3	US-08-557-210A-5
11	864	88.3	193	1	US-08-192-479-2
12	864	88.3	193	1	US-08-637-508-2
13	864	88.3	193	1	US-08-417-791-2
14	864	88.3	193	5	PCI-US96-04546-2
15	864	88.3	297	4	US-10-030-031A-2
16	864	88.3	368	3	US-09-433-428D-58
17	864	88.3	439	3	US-09-433-428D-57
18	862	88.1	186	3	US-09-230-637-37
19	807	82.5	187	3	US-09-230-637-35
20	544.5	55.7	115	6	5164490-6
21	472.5	48.3	210	2	US-08-770-379-1
22	472.5	48.3	210	3	US-09-230-637-23
23	398	40.7	182	3	US-09-230-637-38
24	293.5	30.0	206	6	5164490-1
25	284	28.4	612	4	US-09-203-895-3
26	249	25.5	194	4	US-09-248-796A-20937
27	239	24.4	171	4	US-09-252-991A-27929

28 224 22.9 227 3 US-08-213-419B-13 Sequence 13, Appli  
29 223.5 22.9 168 3 US-08-990-791-9 Sequence 9, Appli  
30 223.5 22.9 168 4 US-09-372-591-9 Sequence 9, Appli  
31 210.5 21.5 197 4 US-09-107-532A-4134 Sequence 4134, Ap  
32 201.5 20.6 165 4 US-09-107-532A-7262 Sequence 7262, Ap  
33 201.5 20.6 165 4 US-09-134-000C-5700 Sequence 5700, Ap  
34 193 19.7 160 3 US-08-990-791-8 Sequence 8, Appli  
35 193 19.7 160 4 US-09-372-591-8 Sequence 8, Appli  
36 186.5 19.1 180 4 US-09-328-352-8063 Sequence 8063, Ap  
37 182.5 18.7 176 4 US-09-540-236-2589 Sequence 2589, Ap  
38 179 18.3 181 3 US-08-990-791-2 Sequence 2, Appli  
39 179 18.3 181 3 US-08-990-791-12 Sequence 12, Appli  
40 179 18.3 181 4 US-09-372-591-2 Sequence 12, Appli  
41 179 18.3 181 4 US-09-372-591-12 Sequence 12, Appli  
42 172 17.6 159 4 US-09-489-039A-12328 Sequence 12328, A  
43 169 17.3 160 3 US-08-809-326A-14 Sequence 14, Appli  
44 169 17.3 160 4 US-09-689-914A-14 Sequence 14, Appli  
45 169 17.3 160 4 US-09-689-913A-14 Sequence 14, Appli

#### ALIGNMENTS

RESULT 1

US-09-142-530C-7

; Sequence 7, Application US/09142530C

; Patent No. 6642043

; GENERAL INFORMATION:

; APPLICANT: Bertino, Joseph R

; APPLICANT: Ericikan-Abali, Emine

; APPLICANT: Banerjee, Debabrata

; APPLICANT: Minsishi, Shin

; APPLICANT: Sadelain, Michel

; TITLE OF INVENTION: Double Mutants of Dihydrofolate Reductase and Methods of Using

; TITLE OF INVENTION: Same

; FILE REFERENCE: MSK.P-007

; CURRENT APPLICATION NUMBER: US/09/142.530C

; PRIOR FILING DATE: 1999-01-20

; PRIOR APPLICATION NUMBER: PCT/US97/03873

; PRIOR FILING DATE: 1997-03-12

; PRIOR APPLICATION NUMBER: US 60/013,270

; PRIOR FILING DATE: 1996-03-12

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: Patent version 3.2

; SEQ ID NO 7

; LENGTH: 186

; TYPE: PRT

; ORGANISM: human

US-09-142-530C-7

Query Match 100.0%; Score 978; DB 4; Length 186;

Best Local Similarity 100.0%; Pred. No. 2.2e-103;

Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VGLNCIVAVSQNMIGKNGDLPWFLRNEFRYQRTMTTSSVEGKQNLVIMGKKTWFSI 60

Db 1 VGLNCIVAVSQNMIGKNGDLPWFLRNEFRYQRTMTTSSVEGKQNLVIMGKKTWFSI 60

Qy 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDALKLTPQPELANKVDWVWVGSSV 120

Db 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDALKLTPQPELANKVDWVWVGSSV 120

Qy 121 YKEAMNHPGHLKLFVTRIMQDPESDTFFPEIDLKYLPPYGVLSVQVEKGIGYKFE 180

Db 121 YKEAMNHPGHLKLFVTRIMQDPESDTFFPEIDLKYLPPYGVLSVQVEKGIGYKFE 180

Qy 181 VYEKND 186

Db 181 VYEKND 186

RESULT 2

US-09-230-637-36

	Sequence 36, Application US/09230637	
	Patent No. 6264958	
	GENERAL INFORMATION:	
	APPLICANT: Hayward, Gary	
	INVENTOR: Nicholas, John	
	ATTORNEY: Hardwick, J. Marie	
	RESEARCHER: Reitz, Marvin	
	TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma	
	FILE REFERENCE: Associated Herpesvirus	
	CURRENT FILING DATE: 1107.78372	
	PRIOR APPLICATION NUMBER: US/09/230.637	
	PRIOR FILING DATE: 1999-11-23	
	PRIOR APPLICATION NUMBER: 60/022.591	
	PRIOR FILING DATE: 1996-07-25	
	PRIOR APPLICATION NUMBER: PCT US 97/12931	
	PRIOR FILING DATE: 1997-07-24	
	NUMBER OF SEQ ID NOS: 62	
	SOFTWARE: FastSeq for Windows Version 4.0	
	SEQ ID NO 36	
	LENGTH: 186	
	TYPE: PRT	
	ORGANISM: Homo sapiens	
	US-09-230-637-36	
	Query Match 97.8%; Score 956; DB 3; Length 186;	
	Best Local Similarity 98.4%; Pred. No. 7.le-101;	
	Matches 183; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	1 VGSNCIVAVSQNMIGKNGDLPWPFLENEPRYFQRMFTTSSVEGKNLVIMGKKTWFSI 60	
DB	1 VGSNCIVAVSQNMIGKNGDLPWPFLENEPRYFQRMFTTSSVEGKNLVIMGKKTWFSI 60	
QY	61 PEKRPPLKGRNLVLSRELKEPPPOGAHFLSRSLDDALKLTPQLANKVDMMVIVGSSV 120	
DB	61 PEKRPPLKGRNLVLSRELKEPPPOGAHFLSRSLDDALKLTPQLANKVDMMVIVGSSV 120	
QY	121 YKEAMNHPGHLLKFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEKGIKYKFE 180	
DB	121 YKEAMNHPGHLLKFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEKGIKYKFE 180	
QY	181 VYEKD 186	
DB	181 VYEKD 186	
	RESULT 3	
	US-09-347-878-28	
	Sequence 28, Application US/09347878C	
	Patent No. 6376210	
	GENERAL INFORMATION:	
	APPLICANT: Yuan, Chong	
	TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES	
	FILE REFERENCE: 25885-1651	
	CURRENT APPLICATION NUMBER: US/09/347.878C	
	CURRENT FILING DATE: 1999-07-06	
	NUMBER OF SEQ ID NOS: 75	
	SOFTWARE: PatentIn Ver. 2.0	
	SEQ ID NO 28	
	LENGTH: 187	
	TYPE: PRT	
	ORGANISM: Cricetus sp.	
	US-09-347-878-28	
	Query Match 91.2%; Score 892; DB 3; Length 187;	
	Best Local Similarity 91.3%; Pred. No. 1.4e-93;	
	Matches 168; Conservative 9; Mismatches 7; Indels 0; Gaps 0;	
QY	1 VGSNCIVAVSQNMIGKNGDLPWPFLENEPRYFQRMFTTSSVEGKNLVIMGKKTWFSI 60	
DB	2 VRPLNCIVAVSQNMIGKNGDLPWPFLENEPRYFQRMFTTSSVEGKNLVIMGKKTWFSI 61	
QY	61 PEKRPPLKGRNLVLSRELKEPPPOGAHFLSRSLDDALKLTPQLANKVDMMVIVGSSV 120	
	Sequence 36, Application US/09230637	
	Patent No. 6264958	
	GENERAL INFORMATION:	
	APPLICANT: Hayward, Gary	
	INVENTOR: Nicholas, John	
	ATTORNEY: Hardwick, J. Marie	
	RESEARCHER: Reitz, Marvin	
	TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma	
	FILE REFERENCE: Associated Herpesvirus	
	CURRENT FILING DATE: 1107.78372	
	PRIOR APPLICATION NUMBER: US/09/230.637	
	PRIOR FILING DATE: 1999-11-23	
	PRIOR APPLICATION NUMBER: 60/022.591	
	PRIOR FILING DATE: 1996-07-25	
	PRIOR APPLICATION NUMBER: PCT US 97/12931	
	PRIOR FILING DATE: 1997-07-24	
	NUMBER OF SEQ ID NOS: 62	
	SOFTWARE: FastSeq for Windows Version 4.0	
	SEQ ID NO 36	
	LENGTH: 186	
	TYPE: PRT	
	ORGANISM: Homo sapiens	
	US-09-230-637-36	
	Query Match 97.8%; Score 956; DB 3; Length 186;	
	Best Local Similarity 98.4%; Pred. No. 7.le-101;	
	Matches 183; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	1 VGSNCIVAVSQNMIGKNGDLPWPFLENEPRYFQRMFTTSSVEGKNLVIMGKKTWFSI 60	
DB	1 VGSNCIVAVSQNMIGKNGDLPWPFLENEPRYFQRMFTTSSVEGKNLVIMGKKTWFSI 60	
QY	61 PEKRPPLKGRNLVLSRELKEPPPOGAHFLSRSLDDALKLTPQLANKVDMMVIVGSSV 120	
DB	61 PEKRPPLKGRNLVLSRELKEPPPOGAHFLSRSLDDALKLTPQLANKVDMMVIVGSSV 120	
QY	121 YKEAMNHPGHLLKFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEKGIKYKFE 180	
DB	121 YKEAMNHPGHLLKFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEKGIKYKFE 180	
QY	181 VYEKD 186	
DB	181 VYEKD 186	
	RESULT 3	
	US-09-347-878-28	
	Sequence 28, Application US/09347878C	
	Patent No. 6376210	
	GENERAL INFORMATION:	
	APPLICANT: Yuan, Chong	
	TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES	
	FILE REFERENCE: 25885-1651	
	CURRENT APPLICATION NUMBER: US/09/347.878C	
	CURRENT FILING DATE: 1999-07-06	
	NUMBER OF SEQ ID NOS: 75	
	SOFTWARE: PatentIn Ver. 2.0	
	SEQ ID NO 28	
	LENGTH: 187	
	TYPE: PRT	
	ORGANISM: Cricetus sp.	
	US-09-347-878-28	
	Query Match 91.2%; Score 892; DB 3; Length 187;	
	Best Local Similarity 91.3%; Pred. No. 1.4e-93;	
	Matches 168; Conservative 9; Mismatches 7; Indels 0; Gaps 0;	
QY	1 VGSNCIVAVSQNMIGKNGDLPWPFLENEPRYFQRMFTTSSVEGKNLVIMGKKTWFSI 60	
DB	2 VRPLNCIVAVSQNMIGKNGDLPWPFLENEPRYFQRMFTTSSVEGKNLVIMGKKTWFSI 61	
QY	61 PEKRPPLKGRNLVLSRELKEPPPOGAHFLSRSLDDALKLTPQLANKVDMMVIVGSSV 120	

Sequence 19, Application US/08761277A  
Patent No. 5972334  
GENERAL INFORMATION:  
APPLICANT: Denney Jr., Dan W.  
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
TITLE OF INVENTION: Leukemia  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/761,277A  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/644,664  
FILING DATE: 01-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: GENITOPE-02406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-00658-3

Query Match 90.0%; Score 880; DB 2; Length 187;  
Best Local Similarity 89.2%; Pred. No. 3.3e-92;  
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNGIGKNGDLPWPFLENEPRYQRMFTTSSVEGKQNLVIMGKKTWFSI 60  
Db 2 VRPLNCIVAVSQNGIGKNGDLPWPFLENEPRYQRMFTTSSVEGKQNLVIMGKKTWFSI 61

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRDLDALKLTPQELANKVDMWVIVGSSV 120  
Db 62 PEKNRPLKDRINVLISRELKEPPRGAHFLAKSLDLDALRLIEQPELASKVDWVIVGSSV 121

QY 121 YKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQBEKGIKYKFE 180  
Db 122 YQEAMNQPGHLKLFVTRIMQDFESDTFFPEIDLGKYKLLPEYPGVLSVQBEKGIKYKFE 181

QY 181 VYEKND 186  
Db 182 VYEKND 187

RESULT 7  
US-08-257-341-9  
Sequence 9, Application US/08257341  
Patent No. 5525491  
GENERAL INFORMATION:  
APPLICANT: HUSTON, JAMES S  
APPLICANT: OPPERMAN, HERMANN  
APPLICANT: TIMASHEFF, SERGE N  
TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CREATIVE BIOMOLECULES, INC./PATENT DEPT.  
STREET: 35 SOUTH STREET  
CITY: HOPKINTON  
STATE: MA  
COUNTRY: USA  
ZIP: 01748  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

Sequence 19, Application US/08761277A  
Patent No. 5972334  
GENERAL INFORMATION:  
APPLICANT: Denney Jr., Dan W.  
TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
TITLE OF INVENTION: Leukemia  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/761,277A  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/644,664  
FILING DATE: 01-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: GENITOPE-02406  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-761-277A-19

Query Match 90.0%; Score 880; DB 2; Length 187;  
Best Local Similarity 89.2%; Pred. No. 3.3e-92;  
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNGIGKNGDLPWPFLENEPRYQRMFTTSSVEGKQNLVIMGKKTWFSI 60  
Db 2 VRPLNCIVAVSQNGIGKNGDLPWPFLENEPRYQRMFTTSSVEGKQNLVIMGKKTWFSI 61

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRDLDALKLTPQELANKVDMWVIVGSSV 120  
Db 62 PEKNRPLKDRINVLISRELKEPPRGAHFLAKSLDLDALRLIEQPELASKVDWVIVGSSV 121

QY 121 YKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQBEKGIKYKFE 180  
Db 122 YQEAMNQPGHLKLFVTRIMQDFESDTFFPEIDLGKYKLLPEYPGVLSVQBEKGIKYKFE 181

QY 181 VYEKND 186  
Db 182 VYEKND 187

RESULT 6  
PCT-US94-00658-3  
Sequence 3, Application PC/TUS9400658  
GENERAL INFORMATION:  
APPLICANT: Dörner, Andrew  
APPLICANT: Fritsch, Edward  
APPLICANT: Steining, Robert  
APPLICANT: Bush, Lawrence  
TITLE OF INVENTION: MCSF-223 Amino Acid Process  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/257,341  
 FILING DATE: 14-NOV-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/842,149  
 FILING DATE: 14-NOV-1994  
 FILING DATE: 27-FEB-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CAMPBELL ESQ, PAULA A  
 REGISTRATION NUMBER: 32,503  
 REFERENCE/DOCKET NUMBER: CRP-064CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/248-7000 (ATTY)  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 471 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-257-341-9

Query Match 89.4%; Score 874; DB 1; Length 471;  
 Best Local Similarity 88.7%; Pred. No. 6.2e-91;  
 Matches 165; Conservative 12; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 VGLNCIVAVSQNMIGKNGDLPWPFLENEPRYFQMTTSSVEGKQNLVIMGKKTWFSI 60  
 DB 2 VRPLNCIVAVSQNMIGKNGDLPWPFLENEPRYFQMTTSSVEGKQNLVIMGKKTWFSI 61  
 QY 61 PEKNPLKGRINVLVLSRELKEPPGGAHPLSRDLDALKLTEQPELANKVDMMVIVGSSV 120  
 DB 62 PEKNPLKDRINIVLSRELKEPPGGAHPLSRDLDALRLIEQPELASKVDMMVIVGSSV 121  
 QY 121 YKEAMNHGHLKLFVTRIMQDFESDTTFPEIDLEKYLLPEYPGVLSDVQBEKGKIKYKFE 180  
 DB 122 YQEANQGHRLFLVTRIMQDFESDTTFPEIDLEKYLLPEYPGVLSDVQBEKGKIKYKFE 181  
 QY 181 VYEKND 186  
 DB 182 VYEKND 187

RESULT 8  
 US-08-557-210A-3  
 Sequence 3, Application US/08557210A  
 Patent No. 6114146  
 GENERAL INFORMATION:  
 APPLICANT: Herlitschka, Sabine  
 APPLICANT: Schlokot, Uwe  
 APPLICANT: Falkner, Falko Guenther  
 APPLICANT: Dörner, Friedrich  
 TITLE OF INVENTION: An expression plasmid, a fusion protein, a  
 TITLE OF INVENTION: transfected eukaryotic cell line, a method of producing foreign  
 TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmaceu  
 TITLE OF INVENTION: composition  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/557,210A  
 FILING DATE: 14-NOV-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: A 2099/94  
 FILING DATE: 14-NOV-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ISACSON, John P.  
 REGISTRATION NUMBER: 33,715  
 REFERENCE/DOCKET NUMBER: 040433/0142/SOPA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEFAX: (202)672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 524 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-557-210A-3

Query Match 89.4%; Score 874; DB 3; Length 524;  
 Best Local Similarity 89.7%; Pred. No. 7.2e-91;  
 Matches 165; Conservative 12; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 VGLNCIVAVSQNMIGKNGDLPWPFLENEPRYFQMTTSSVEGKQNLVIMGKKTWFSI 60  
 DB 2 VRPLNCIVAVSQNMIGKNGDLPWPFLENEPRYFQMTTSSVEGKQNLVIMGKKTWFSI 61  
 QY 61 PEKNPLKGRINVLVLSRELKEPPGGAHPLSRDLDALKLTEQPELANKVDMMVIVGSSV 120  
 DB 62 PEKNPLKDRINIVLSRELKEPPGGAHPLSRDLDALRLIEQPELASKVDMMVIVGSSV 121  
 QY 121 YKEAMNHGHLKLFVTRIMQDFESDTTFPEIDLEKYLLPEYPGVLSDVQBEKGKIKYKFE 180  
 DB 122 YQEANQGHRLFLVTRIMQDFESDTTFPEIDLEKYLLPEYPGVLSDVQBEKGKIKYKFE 181  
 QY 181 VYEK 184  
 DB 182 VYEK 185

RESULT 9  
 US-08-557-210A-4  
 Sequence 4, Application US/08557210A  
 Patent No. 6114146  
 GENERAL INFORMATION:  
 APPLICANT: Herlitschka, Sabine  
 APPLICANT: Schlokot, Uwe  
 APPLICANT: Falkner, Falko Guenther  
 APPLICANT: Dörner, Friedrich  
 TITLE OF INVENTION: An expression plasmid, a fusion protein, a  
 TITLE OF INVENTION: transfected eukaryotic cell line, a method of producing foreign  
 TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmaceu  
 TITLE OF INVENTION: composition  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/557,210A

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/
/ FILING DATE: 14-NOV-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: A 2099/94
/ FILING DATE: 14-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ISACSON, John P.
/ REGISTRATION NUMBER: 33,715
/ REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 539 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 192..196
/ OTHER INFORMATION: /note= "Glycin Spacer"
/
US-08-557-210A-4

Query Match 89.4%; Score 874; DB 3; Length 539;
Best Local Similarity 89.7%; Pred. No. 7.5e-91;
Matches 165; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VGSNCIVAVSONMGIGKNGDLPWFLRNEPRYFORMTTSSVEGKQNLVIMGKKTWFSI 60
Db 2 VRPLNCIVAVSONMGIGKNGDLPWFLRNEPRYFORMTTSSVEGKQNLVIMGKKTWFSI 61
Qy 61 PEKNRPLKGRINVLISRELKEPPQGAHFLSRSLDALKLTPQELANKYDVMWIVGGSSV 120
Db 62 PEKNRPLKDRINVLISRELKEPPRGAFHFLAKSLDALKLIEQELASKYDVMWIVGGSSV 121
Qy 121 YKEAMNHGHLKLFVTRIMQFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKFE 180
Db 122 YQEAMNQGHRLFLVTRIMQFESDTFFPEIDLGKYLLEPYPGVLSDVQEEKGIKYKFE 181
Qy 181 VYEK 184
Db 182 VYEK 185

RESULT 10
US-08-557-210A-5
/ Sequence 5, Application US/08557210A
/ Patent No. 6114146
/ GENERAL INFORMATION:
/ APPLICANT: Herlitschka, Sabine
/ APPLICANT: Schlokot, Uwe
/ APPLICANT: Falkner, Falko Guenther
/ APPLICANT: Dornier, Friedrich
/ TITLE OF INVENTION: An expression plasmid, a fusion protein, a
/ TITLE OF INVENTION: transfected eukaryotic cell line, a method of producing foreign
/ TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmaceu
/ TITLE OF INVENTION: composition
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/557,210A
/ FILING DATE: 14-NOV-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: A 2099/94
/ FILING DATE: 14-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ISACSON, John P.
/ REGISTRATION NUMBER: 33,715
/ REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 539 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Peptide
/ LOCATION: 190..194
/ OTHER INFORMATION: /note= "Prolin Spacer"
/
US-08-557-210A-5

Query Match 89.4%; Score 874; DB 3; Length 539;
Best Local Similarity 89.7%; Pred. No. 7.5e-91;
Matches 165; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 VGSNCIVAVSONMGIGKNGDLPWFLRNEPRYFORMTTSSVEGKQNLVIMGKKTWFSI 60
Db 2 VRPLNCIVAVSONMGIGKNGDLPWFLRNEPRYFORMTTSSVEGKQNLVIMGKKTWFSI 61
Qy 61 PEKNRPLKGRINVLISRELKEPPQGAHFLSRSLDALKLTPQELANKYDVMWIVGGSSV 120
Db 62 PEKNRPLKDRINVLISRELKEPPRGAFHFLAKSLDALKLIEQELASKYDVMWIVGGSSV 121
Qy 121 YKEAMNHGHLKLFVTRIMQFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKFE 180
Db 122 YQEAMNQGHRLFLVTRIMQFESDTFFPEIDLGKYLLEPYPGVLSDVQEEKGIKYKFE 181
Qy 181 VYEK 184
Db 182 VYEK 185

RESULT 11
US-08-192-479-2
/ Sequence 2, Application US/08192479
/ Patent No. 5538862
/ GENERAL INFORMATION:
/ APPLICANT: Wu, Peipei
/ APPLICANT: Dohmen, Jurgen
/ APPLICANT: Johnston, Jennifer
/ APPLICANT: Varshavsky, Alexander
/ TITLE OF INVENTION: HEAT-INDUCIBLE N-DEGRON
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kevin M. Farrell
/ STREET: P.O. Box 999
/ CITY: York Harbor
/ STATE: Maine
/ COUNTRY: USA
/ ZIP: 03911
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/192,479

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Farrell, Kevin M.

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: CIT9301

TELEPHONE: (207) 363-0558

TELEFAX: (207) 363-0528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-192-479-2

Query Match 88.3%; Score 864; DB 1; Length 193;

Best Local Similarity 88.2%; Pred. No. 2.3e-90;

Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSONMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60

DB 8 VRPLNCIVAVSONMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 67

QY 61 PEKNRPLKGRINVLVLSRELKEPPQGAHFLSRSLDALKLITEQPELANKVDWVWIVGGSSV 120

DB 68 PEKNRLLKDRINVLVLSRELKEPPQGAHFLSRSLDALKLITEQPELANKVDWVWIVGGSSV 127

QY 121 YXEAMNHPGHLKLFVTRINQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEKGIKYKFE 180

DB 128 YQEMNQGHLLFVTRINQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEKGIKYKFE 187

QY 181 VYEKND 186

DB 188 VYEKND 193

RESULT 12

US-08-637-508-2

Sequence 2, Application US/08637508

Patent No. 5705387

GENERAL INFORMATION:

APPLICANT: Wu, Peipei

APPLICANT: Dohmen, Jurgen

APPLICANT: Varshavsky, Alexander

TITLE OF INVENTION: HEAT-INDUCIBLE N-DEGRON

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell

STREET: P.O. Box 999

CITY: York Harbor

STATE: Maine

COUNTRY: USA

ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/637,508

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/192,479

FILING DATE: 04-FEB-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Farrell, Kevin M.

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: CIT9301D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558

TELEFAX: (207) 363-0528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-637-508-2

Query Match 88.3%; Score 864; DB 1; Length 193;

Best Local Similarity 88.2%; Pred. No. 2.3e-90;

Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSONMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60

DB 8 VRPLNCIVAVSONMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 67

QY 61 PEKNRPLKGRINVLVLSRELKEPPQGAHFLSRSLDALKLITEQPELANKVDWVWIVGGSSV 120

DB 68 PEKNRLLKDRINVLVLSRELKEPPQGAHFLSRSLDALKLITEQPELANKVDWVWIVGGSSV 127

QY 121 YXEAMNHPGHLKLFVTRINQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEKGIKYKFE 180

DB 128 YQEMNQGHLLFVTRINQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEKGIKYKFE 187

QY 181 VYEKND 186

DB 188 VYEKND 193

RESULT 13

US-08-417-791-2

Sequence 2, Application US/08417791

Patent No. 5763212

GENERAL INFORMATION:

APPLICANT: Johnston, Jennifer

APPLICANT: Varshavsky, Alexander

TITLE OF INVENTION: HEAT-INDUCIBLE N-DEGRON

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell

STREET: P.O. Box 999

CITY: York Harbor

STATE: Maine

COUNTRY: USA

ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,791

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/192,479

FILING DATE: 04-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Farrell, Kevin M.

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: CIT9301

TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558

TELEFAX: (207) 363-0528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 193 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein



US-08-417-791-2

Query Match 88.3%; Score 864; DB 1; Length 193;  
Best Local Similarity 88.2%; Pred. No. 2.3e-90;  
Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPPFLRNEFRYQRMVTTSSVEGKQNLVIMGKKTWFSI 60  
DB 8 VRPLNCIVAVSQNMIGKNGDLPPFLRNEFRYQRMVTTSSVEGKQNLVIMGKKTWFSI 67

QY 61 PEKNRPLKGRINVLRSRELKPPQGAHFLSRSLDDALKLTEQPELANKVDMVWIVGGSSV 120  
DB 68 PEKNRLLKDRINIVLSRELKPPQGAHFLAKSLDDALRLIEQPELASKVDMVWIVGGSSV 127

QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEKGIKYKFE 180  
DB 128 YQEAMNQPHLRLFVTRIMQDFESDTFFPEIDLGKYLPEYPGVLSVQVEKGIKYKFE 187

QY 181 VYEKND 186  
DB 188 VYEKXD 193

RESULT 14

PCT-US96-04546-2

; Sequence 2, Application PC/TUS9604546  
; GENERAL INFORMATION:  
; APPLICANT: California Institute of Technology  
; TITLE OF INVENTION: HEAT-INDUCIBLE N-DEGRON  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kevin M. Farrell  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: Maine  
; COUNTRY: USA  
; ZIP: 03911

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/04546  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/417,791  
; FILING DATE: 06-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farrell, Kevin M.  
; REGISTRATION NUMBER: 35,505  
; REFERENCE/DOCKET NUMBER: CIT9301A WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (207) 363-0558  
; TELEFAX: (207) 363-0528  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US96-04546-2

Query Match 88.3%; Score 864; DB 5; Length 193;  
Best Local Similarity 88.2%; Pred. No. 2.3e-90;  
Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPPFLRNEFRYQRMVTTSSVEGKQNLVIMGKKTWFSI 60  
DB 8 VRPLNCIVAVSQNMIGKNGDLPPFLRNEFRYQRMVTTSSVEGKQNLVIMGKKTWFSI 67

QY 61 PEKNRPLKGRINVLRSRELKPPQGAHFLSRSLDDALKLTEQPELANKVDMVWIVGGSSV 120

DB 68 PEKNRLLKDRINIVLSRELKPPQGAHFLAKSLDDALRLIEQPELASKVDMVWIVGGSSV 127

QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEKGIKYKFE 180  
DB 128 YQEAMNQPHLRLFVTRIMQDFESDTFFPEIDLGKYLPEYPGVLSVQVEKGIKYKFE 187

QY 181 VYEKND 186  
DB 188 VYEKXD 193

RESULT 15

US-10-030-031A-2

; Sequence 2, Application US/100300031A  
; Patent No. 6746847  
; GENERAL INFORMATION:  
; APPLICANT: Vermeer, Ceas  
; TITLE OF INVENTION: Diagnostic Assay for Human Matrix  
; FILE REFERENCE: 13176PCTUS  
; CURRENT APPLICATION NUMBER: US/10/030,031A  
; PRIOR FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: PCT/EP00/06173  
; PRIOR FILING DATE: 2000-07-02  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 297  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Protein encoded by Sequence 1 containing 6-His tag  
; Patent No. 6746847  
; OTHER INFORMATION: - DHFR - linker (=4 amino acids) - MGP

US-10-030-031A-2

Query Match 88.3%; Score 864; DB 4; Length 297;  
Best Local Similarity 89.1%; Pred. No. 4.3e-90;  
Matches 164; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPPFLRNEFRYQRMVTTSSVEGKQNLVIMGKKTWFSI 60  
DB 16 VRPLNSIVAVSQNMIGKNGDLPPFLRNEFRYQRMVTTSSVEGKQNLVIMGKKTWFSI 75

QY 61 PEKNRPLKGRINVLRSRELKPPQGAHFLSRSLDDALKLTEQPELANKVDMVWIVGGSSV 120  
DB 76 PEKNRLLKDRINIVLSRELKPPQGAHFLAKSLDDALRLIEQPELASKVDMVWIVGGSSV 135

QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQVEKGIKYKFE 180  
DB 136 YQEAMNQPHLRLFVTRIMQDFESDTFFPEIDLGKYLPEYPGVLSVQVEKGIKYKFE 195

QY 181 VYEK 184  
DB 196 VYEK 199

Search completed: November 19, 2004, 13:53:27  
Job time : 40 secs



Result No.	Query			Description	
	Score	Match	Length	ID	Description
1	978	100.0	186	15	US-10-421-285-5
2	968	99.0	187	17	US-10-733-878-503
3	880	90.0	187	9	US-09-925-664-19
4	880	90.0	187	11	US-09-925-192-19
5	878	89.8	187	15	US-10-421-285-3
6	867	89.7	187	15	US-10-381-898-8
7	864	88.3	297	17	US-10-832-734-2
8	862	88.1	187	15	US-10-421-285-4
9	587.5	60.1	188	15	US-10-421-285-2
10	319.5	32.7	189	14	US-10-369-493-5158
11	301	30.8	530	15	US-10-424-599-247813
12	300	30.7	579	15	US-10-425-114-49649
13	298	30.5	475	15	US-10-425-114-43022

121 YKEAMNHPGHLKLFVTRIMODFESDTFFPEIDLEKYKLLPEYPGVLSVDOEEKGIKYKFE 180

Sequence 197466,  
Sequence 247817,  
Sequence 125793,  
Sequence 3987, Ap  
Sequence 295031,  
Sequence 14308,  
Sequence 14586, A  
Sequence 1438, A  
Sequence 14938,  
Sequence 11559,  
Sequence 13912, A  
Sequence 11779, A  
Sequence 65164, A  
Sequence 17427, A  
Sequence 289105,  
Sequence 22402, A  
Sequence 8688, Ap  
Sequence 70130,  
Sequence 19656,  
Sequence 57433,  
Sequence 7697,  
Sequence 50482, A  
Sequence 16949,  
Sequence 37727, A  
Sequence 16480,  
Sequence 65425,  
Sequence 49091, A  
Sequence 4315, Ap  
Sequence 7072, Ap  
Sequence 19156, A  
Sequence 66094, A  
Sequence 11477, A  
Sequence 58345, A

121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSDVQBEKGIKYKFE 180  
181 VYEKND 186  
181 VYEKND 186

## RESULT 2

US-09-925-664-19  
Sequence 503, Application US/10733878  
Publication No. US20040224408A1  
GENERAL INFORMATION:  
APPLICANT: Jean-Philippe Girard  
APPLICANT: Francois Analtic  
APPLICANT: Myriam Rousigne  
APPLICANT: Thomas Clouaire  
TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR  
TITLE OF INVENTION: CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL  
TITLE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION  
FILE REFERENCE: BIOBANK 012A  
CURRENT APPLICATION NUMBER: US/10/733,878  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: 60/432699  
PRIOR FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: 60/485027  
PRIOR FILING DATE: 2003-07-03  
NUMBER OF SEQ ID NOS: 535  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 503  
LENGTH: 187  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-733-878-503

Query Match 99.0%; Score 968; DB 17; Length 187;  
Best Local Similarity 99.5%; Pred. No. 5.9e-92;  
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 VGSNCIVAVSQNMGIKNGKGLPWFPLRNEFRYFQRMITTSVVEGKQNLVIMGKKTWFSI 60  
2 VGSNCIVAVSQNMGIKNGKGLPWFPLRNEFRYFQRMITTSVVEGKQNLVIMGKKTWFSI 61  
61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTPQELANKVDVWVIVGGSSV 120  
62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTPQELANKVDVWVIVGGSSV 121  
121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSDVQBEKGIKYKFE 180  
122 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSDVQBEKGIKYKFE 181  
181 VYEKND 186  
182 VYEKND 187

## RESULT 3

US-09-925-664-19  
Sequence 19, Application US/09925664  
Patent No. US2002016006A1  
GENERAL INFORMATION:  
APPLICANT: Denney, Jr., Dan W.  
TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia  
FILE REFERENCE: GENITOP-06499  
CURRENT APPLICATION NUMBER: US/09/925,664  
CURRENT FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/370,453  
PRIOR FILING DATE: 1999-08-09  
PRIOR APPLICATION NUMBER: 08/644,664  
PRIOR FILING DATE: 1996-05-01  
PRIOR APPLICATION NUMBER: 08/761,277  
PRIOR FILING DATE: 1996-12-06  
NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19  
LENGTH: 187  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-925-664-19

Query Match 90.0%; Score 880; DB 9; Length 187;  
Best Local Similarity 89.2%; Pred. No. 7.9e-83;  
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;  
1 VGSNCIVAVSQNMGIKNGKGLPWFPLRNEFRYFQRMITTSVVEGKQNLVIMGKKTWFSI 60  
2 VRLNCIVAVSQNMGIKNGKGLPWFPLRNEFRYFQRMITTSVVEGKQNLVIMGKKTWFSI 61  
61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTPQELANKVDVWVIVGGSSV 120  
62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTPQELANKVDVWVIVGGSSV 121  
121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSDVQBEKGIKYKFE 180  
122 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSDVQBEKGIKYKFE 181  
181 VYEKND 186  
182 VYEKND 187

## RESULT 4

US-09-925-192-19  
Sequence 19, Application US/09925192  
Publication No. US20040096452A1  
GENERAL INFORMATION:  
APPLICANT: Denney, Jr., Dan W.  
TITLE OF INVENTION: Vaccines for Treatment of Lymphoma and Leukemia  
FILE REFERENCE: GENITOP-06493  
CURRENT APPLICATION NUMBER: US/09/925,192  
CURRENT FILING DATE: 2001-08-09  
NUMBER OF SEQ ID NOS: 80  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 19  
LENGTH: 187  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-925-192-19

Query Match 90.0%; Score 880; DB 11; Length 187;  
Best Local Similarity 89.2%; Pred. No. 7.9e-83;  
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;  
1 VGSNCIVAVSQNMGIKNGKGLPWFPLRNEFRYFQRMITTSVVEGKQNLVIMGKKTWFSI 60  
2 VRLNCIVAVSQNMGIKNGKGLPWFPLRNEFRYFQRMITTSVVEGKQNLVIMGKKTWFSI 61  
61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTPQELANKVDVWVIVGGSSV 120  
62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDDALKLTPQELANKVDVWVIVGGSSV 121  
121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSDVQBEKGIKYKFE 180  
122 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYGVLSDVQBEKGIKYKFE 181  
181 VYEKND 186  
182 VYEKND 187

## RESULT 5

US-10-421-285-3  
Sequence 3, Application US/10421285  
Publication No. US20040053836A1  
GENERAL INFORMATION:  
APPLICANT: Mayerkuckuk, Phillip

APPLICANT: Banerjee, Debabrata  
APPLICANT: Bertino, Joseph R.  
TITLE OF INVENTION: Method for Modulating the Production of a Selected Protein In  
TITLE OF INVENTION: Vivo  
FILE REFERENCE: MSK-P-053  
CURRENT APPLICATION NUMBER: US/10/421,285  
CURRENT FILING DATE: 2003-04-22  
PRIOR APPLICATION NUMBER: US 60/375,250  
PRIOR FILING DATE: 2002-04-22  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3  
LENGTH: 187  
TYPE: PRT  
ORGANISM: rat  
US-10-421-285-3

Query Match 89.8%; Score 878; DB 15; Length 187;  
Best Local Similarity 88.7%; Pred. No. 1.3e-82;  
Matches 165; Conservative 12; Mismatches 9; Indels 0; Gaps 0;  
QY 1 VGSNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60  
Db 2 VRPLNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 61  
QY 61 PEKNRPLKGRINLVLSRELKPEPQGAHFLSRSLDDALKLTPQELANKVDMWIVGGSSV 120  
Db 62 PEKNRPLKGRINLVLSRELKPEPQGAHFLSRSLDDALKLTPQELANKVDMWIVGGSSV 121  
QY 121 YKEANHPGHLKLFVTRIMQDPESDTFFPEIDLEKYKLLPEYGVLSVQEEKIKYKFE 180  
Db 122 YQEANHPGHLKLFVTRIMQDPESDTFFPEIDLEKYKLLPEYGVLSVQEEKIKYKFE 181  
QY 181 VYEKND 186  
Db 182 VYEKND 187

## RESULT 6

US-10-381-898-8  
Sequence 8, Application US/10381898  
Publication No. US2004008687A1  
GENERAL INFORMATION:  
APPLICANT: AZIMZAI, Valda; BAUGHN, Mariah R.;  
APPLICANT: BOROWSKY, Mark L.; DING, Li;  
APPLICANT: DUGGAN, Brendan; ELIOTT, Vicki S.;  
APPLICANT: GANDHI, Aneena R.; GRIFFIN, Jennifer A.;  
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;  
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;  
APPLICANT: LEE, Ernestine A.; LU, Dyung Aina M.;  
APPLICANT: ARVIZU, Chandra S.; POLICKY, Jennifer L.;  
APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;  
APPLICANT: SANJANWALA, Madhusudan M.;  
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.;  
APPLICANT: CHAWLA, Narinder K.; WALSH, Roderick T.;  
APPLICANT: WARREN, Bridget; XU, Yuming;  
APPLICANT: YANG, Junming; YAO, Monique; YUE, Henry  
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES  
FILE REFERENCE: PI-0233 USN  
CURRENT APPLICATION NUMBER: US/10/381,898  
CURRENT FILING DATE: 2003-10-17  
PRIOR APPLICATION NUMBER: PCT/US01/30662  
PRIOR FILING DATE: 2001-09-28  
PRIOR APPLICATION NUMBER: US 60/236,947  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: US 60/238,864  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 60/242,323  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: US 60/247,581  
PRIOR FILING DATE: 2000-11-09  
PRIOR APPLICATION NUMBER: US 60/249,519  
PRIOR FILING DATE: 2000-11-16

PRIOR APPLICATION NUMBER: US 60/252,834  
PRIOR FILING DATE: 2000-11-22  
PRIOR APPLICATION NUMBER: US 60/250,567  
PRIOR FILING DATE: 2000-11-30  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PERL Program  
SEQ ID NO 8  
LENGTH: 187  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No: 5521346CD1  
US-10-381-898-8

Query Match 88.7%; Score 867; DB 15; Length 187;  
Best Local Similarity 92.3%; Pred. No. 1.7e-81;  
Matches 169; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
QY 4 LNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSIPEK 63  
Db 5 LNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSIPEK 64  
QY 64 NRPLKGRINLVLSRELKPEPQGAHFLSRSLDDALKLTPQELANKVDMWIVGGSSVYKE 123  
Db 65 NRPLKGRINLVLSRELKPEPQGAHFLSRSLDDALKLTPQELANKVDMWIVGGSSVYKE 124  
QY 124 AMNHPGHLKLFVTRIMQDPESDTFFPEIDLEKYKLLPEYGVLSVQEEKIKYKFEVYE 183  
Db 125 AMNHPGHLKLFVTRIMQDPESDTFFPEIDLEKYKLLPEYGVLSVQEEKIKYKFEVCE 184  
QY 184 KND 186  
Db 185 KDD 187

## RESULT 7

US-10-832-734-2  
Sequence 2, Application US/10832734  
Publication No. US20040197830A1  
GENERAL INFORMATION:  
APPLICANT: Vermeer, Cees  
TITLE OF INVENTION: Diagnostic Assay for Human Matrix  
FILE REFERENCE: 13176PCTUS  
CURRENT APPLICATION NUMBER: US/10/832,734  
CURRENT FILING DATE: 2004-04-26  
PRIOR APPLICATION NUMBER: US/10/030,031A  
PRIOR FILING DATE: 2002-07-16  
PRIOR APPLICATION NUMBER: PCT/EP00/06173  
PRIOR FILING DATE: 2000-07-02  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Protein encoded by Sequence 1 containing 6-His tag  
OTHER INFORMATION: - DHFR - linker (=4 amino acids) - MGF  
US-10-832-734-2

Query Match 88.3%; Score 864; DB 17; Length 297;  
Best Local Similarity 89.1%; Pred. No. 6.7e-81;  
Matches 164; Conservative 12; Mismatches 8; Indels 0; Gaps 0;  
QY 1 VGSNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60  
Db 16 VRPLNCIVAVSQNMIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 75  
QY 61 PEKNRPLKGRINLVLSRELKPEPQGAHFLSRSLDDALKLTPQELANKVDMWIVGGSSV 120  
Db 76 PEKNRPLKGRINLVLSRELKPEPQGAHFLSRSLDDALKLTPQELANKVDMWIVGGSSV 135

QY 121 YKEAMNHGHLKLFVTRIMQDPESTFFPEIDLEKYKLLPEYPGVLSVQVEKGKYYKE 180  
DB 136 YCEAMNQPHLKFVTRIMQDPESTFFPEIDLGKYLPEYPGVLSVQVEKGKYYKE 195

QY 181 VYEK 184  
DB 196 VYEK 199

## RESULT 8

US-10-421-285-4  
Sequence 4, Application US/10421285  
Publication No. US20040053836A1  
GENERAL INFORMATION:  
APPLICANT: MayerKuckuk, Phillip  
APPLICANT: Banerjee, Debabrata  
APPLICANT: Bertino, Joseph R.  
TITLE OF INVENTION: Method for Modulating the Production of a Selected Protein In Vivo  
FILE OF INVENTION: MSK.P-053  
FILE REFERENCE: MSK.P-053  
CURRENT APPLICATION NUMBER: US/10/421,285  
PRIOR FILING DATE: 2003-04-22  
PRIOR APPLICATION NUMBER: US 60/375,250  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 4  
LENGTH: 187  
TYPE: PRT  
ORGANISM: mouse  
US-10-421-285-4

Query Match 88.1%; Score 862; DB 15; Length 187;  
Best Local Similarity 88.2%; Pred. No. 5.8e-81;  
Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNMGIGKNGDLPWFLNRPYFORMTTTSSVEGKQNLVIMGKKTWFSI 60  
DB 2 VRLPLNCIVAVSQNMGIGKNGDLPWFLNRPYFORMTTTSSVEGKQNLVIMGKKTWFSI 61  
QY 61 PEKNPLKGRINLVLSRELKEPPQGAHFLSLDDALKTQPELANKVDVMWIVGSSV 120  
DB 62 PEKNPLKGRINLVLSRELKEPPQGAHFLSLDDALKTQPELANKVDVMWIVGSSV 121  
QY 121 YKEAMNHGHLKLFVTRIMQDPESTFFPEIDLEKYKLLPEYPGVLSVQVEKGKYYKE 180  
DB 122 YCEAMNQPHLKFVTRIMQDPESTFFPEIDLGKYLPEYPGVLSVQVEKGKYYKE 181

QY 181 VYEKND 186  
DB 182 VYEKXD 187

## RESULT 9

US-10-421-285-2  
Sequence 2, Application US/10421285  
Publication No. US20040053836A1  
GENERAL INFORMATION:  
APPLICANT: MayerKuckuk, Phillip  
APPLICANT: Banerjee, Debabrata  
APPLICANT: Bertino, Joseph R.  
TITLE OF INVENTION: Method for Modulating the Production of a Selected Protein In Vivo  
FILE OF INVENTION: MSK.P-053  
FILE REFERENCE: MSK.P-053  
CURRENT APPLICATION NUMBER: US/10/421,285  
PRIOR FILING DATE: 2003-04-22  
PRIOR APPLICATION NUMBER: US 60/375,250  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 2  
LENGTH: 188

; TYPE: PRT  
; ORGANISM: monkey  
US-10-421-285-2

Query Match 60.1%; Score 587.5; DB 15; Length 188;  
Best Local Similarity 58.2%; Pred. No. 1.7e-52;  
Matches 107; Conservative 34; Mismatches 40; Indels 3; Gaps 2;

QY 3 SLNCIVAVSQNMGIGKNGDLPWFLNRPYFORMTTTSSVEGKQNLVIMGKKTWFSIPE 62  
DB 4 AVNCIVAVDEQLGIGKNGTMPWFLNRPYFORMTTSTPSVVGKQNVIMGKKTWFSIPE 63  
QY 63 KRPPLKGRINLVLSRELKEPPQGAHFLSLDDALKTQPELANKVDVMWIVGSSVYK 122  
DB 64 KRPPLNRIILVLSRELKEPPQGAHFLSLDDALKTQPELANKVDVMWIVGSSVYK 123  
QY 123 EAMNHGHLKLFVTRIMQDPESTFFPEIDLEKYKLLPEYPGVLSVQVEKGKYYKE 181  
DB 124 SVLNYKCPKLKLVTRIMQDPESTFFPEIDLEKYKLLPEYPGVLSVQVEKGKYYKE 181  
QY 182 YEK 185  
DB 182 YEK 185

## RESULT 10

US-10-369-493-5158  
Sequence 5158, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 5158  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-10-369-493-5158

Query Match 32.7%; Score 319.5; DB 14; Length 189;  
Best Local Similarity 36.0%; Pred. No. 1e-24;  
Matches 64; Conservative 41; Mismatches 70; Indels 3; Gaps 2;

QY 4 LNCIVAVSQNMGIGKNGDLPWFLNRPYFORMTTTSSVEGKQNLVIMGKKTWFSIPEK 63  
DB 4 MNDIVAMDREGGIGKNGVLPWR-IRKMQYFASVTNVSQSKRNAVLNMGKCKWESIPVT 62  
QY 64 NRPLKGRINLVLSRELKEPPQGAHFLSLDDALKTQPELANKVDVMWIVGSSVYK 123  
DB 63 RRPLAGRLNVLRSQLPACKSDDIYVANSLEAAKLLSEPPVDSIETINWIGGAEIYDL 122  
QY 124 AMNHGHLKLFVTRIMQDPESTFFPEIDLEKYKLL--PEYPGVLSVQVEKGKYYKE 179  
DB 123 ALRNLVDEIHLTRIPKFNFEADVHLKSLDFSKQEKVQNAEVSSEISEFENGLAFEP 180

## RESULT 11

US-10-424-599-247813  
Sequence 247813, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 247813  
; LENGTH: 530  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_WRT3847\_65805C.1.pep  
US-10-424-599-247813

Query Match 30.8%; Score 301; DB 15; Length 530;  
Best Local Similarity 33.2%; Pred. No. 3.3e-22;  
Matches 66; Conservative 41; Mismatches 62; Indels 30; Gaps 5;

QY 2 GSLN-----CIVAVSQNMGIKNGDLPWPFLENERFYFORMTTSSVEGKQNLVI 51  
DB 15 GSVNPLNLTQYQVVAAQDWGIGKDGKLPWR-LPTDLKFFKEITMKTSEPGKNAIV 73  
QY 52 MGKKTWFSIPEKNRPLKGRINLVLSRELKEPPOGAHFLSR-----SLDDALKLTEQP 103  
DB 74 MGRKTWESIPEYRPLSGRLNVLTR-----SGSFDIATAENVVIGSGMSALELLAAS 127  
QY 104 ELANKVDVWIVGSSVYKEAMNHPGHLKLFVTRIMQDFESDTPFPEIDLEKYKLLPEYP 163  
DB 128 PYSLSIEKVFVIGGGQIFREALNVPGCCAIHLTEIQSSIECDTFMPPVDFTFIFR-----P 182  
QY 164 GVLSDVQVEEKGIKYKFEVY 182  
DB 183 WYSSFPKVENNIRYSFTTY 201

RESULT 12  
US-10-425-114-49649  
; Sequence 49649, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 49649  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3051-050-G2\_FLI.pep  
US-10-425-114-49649

Query Match 30.7%; Score 300; DB 15; Length 579;  
Best Local Similarity 33.2%; Pred. No. 4.8e-22;  
Matches 66; Conservative 41; Mismatches 62; Indels 30; Gaps 5;

QY 2 GSLN-----CIVAVSQNMGIKNGDLPWPFLENERFYFORMTTSSVEGKQNLVI 51  
DB 64 GSVNPLNLTQYQVVAAQDWGIGKDGKLPWR-LPTDLKFFKEITMKTSEPGKNAIV 122  
QY 52 MGKKTWFSIPEKNRPLKGRINLVLSRELKEPPOGAHFLSR-----SLDDALKLTEQP 103  
DB 123 MGRKTWESIPEYRPLSGRLNVLTR-----SGSFDIATAENVVIGSGMSALELLAAS 176

QY 104 ELANKVDVWIVGSSVYKEAMNHPGHLKLFVTRIMQDFESDTPFPEIDLEKYKLLPEYP 163  
DB 177 PYSLSIEKVFVIGGGQIFREALNVPGCCAIHLTEIQSSIECDTFMPPVDFTFIFR-----P 231  
QY 164 GVLSDVQVEEKGIKYKFEVY 182  
DB 232 WYSSFPKVENNIRYSFTTY 250

## RESULT 13

US-10-425-114-43022  
; Sequence 43022, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 43022  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700746445\_FLI.pep  
US-10-425-114-43022

Query Match 30.5%; Score 298; DB 15; Length 475;

Best Local Similarity 33.2%; Pred. No. 5.9e-22;  
Matches 66; Conservative 41; Mismatches 62; Indels 30; Gaps 5;

QY 2 GSLN-----CIVAVSQNMGIKNGDLPWPFLENERFYFORMTTSSVEGKQNLVI 51  
DB 85 GSVNPLNLTQYQVVAAQDWGIGKDGKLPWR-LPTDLKFFKEITMKTSEPGKNAIV 143  
QY 52 MGKKTWFSIPEKNRPLKGRINLVLSRELKEPPOGAHFLSR-----SLDDALKLTEQP 103  
DB 144 MGRKTWESIPEYRPLSGRLNVLTR-----SGSFDIATAENVVIGSGMSALELLAAS 197  
QY 104 ELANKVDVWIVGSSVYKEAMNHPGHLKLFVTRIMQDFESDTPFPEIDLEKYKLLPEYP 163  
DB 198 PYSLSIEKVFVIGGGQIFREALNVPGCCAIHLTEIQSSIECDTFMPPVDFTFIFR-----P 252  
QY 164 GVLSDVQVEEKGIKYKFEVY 182  
DB 253 WYSSFPKVENNIRYSFTTY 271

## RESULT 14

US-10-437-963-197466  
; Sequence 197466, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963

188 PLV-----EDNLRYSFTTY 201

188 PLV-----EDNLRYSFTTY 201





A:Description: catalyzes the reduction of dihydrofolic acid to tetrahydrofolic acid with  
 A:Pathway: tetrahydrofolate synthesis  
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology  
 C:Species: Cricetus griseus (Chinese hamster)  
 C:Keywords: NADP; oxidoreductase  
 E:2-187/Product: dihydrofolate reductase #status experimental <MAT>  
 F:4-126/Domain: type I dihydrofolate reductase homology <DPR>  
 F:31,35,64,71/Binding site: substrate (Glu, Phe, Asn, Arg) #status experimental

Query Match 99.0%; Score 968; DB 1; Length 187;  
 Best Local Similarity 99.5%; Pred. No. 1e-77; Indels 0; Gaps 0;  
 Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNGIGKNGDLPWPLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI 60  
 DB 2 VGLNCIVAVSQNGIGKNGDLPWPLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI 61  
 QY 61 PEKNRPLKGRINLVLSRELKEPQGAHFLSLDLDALKEPELANKVDWVWIVGGSSV 120  
 DB 62 PEKNRPLKGRINLVLSRELKEPQGAHFLSLDLDALKEPELANKVDWVWIVGGSSV 121  
 QY 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 180  
 DB 122 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 181  
 QY 181 VYEKND 186  
 DB 182 VYEKND 187

RESULT 2  
 QY75  
 A:Description: catalyzes the reduction of dihydrofolic acid to tetrahydrofolic acid with  
 A:Pathway: tetrahydrofolate synthesis  
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology  
 C:Species: Cricetus griseus (Chinese hamster)  
 C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 16-Aug-2004  
 C:Accession: A28274; I48104  
 R:Melera, P.W.; Davide, J.P.; Oen, H.  
 J. Biol. Chem. 263, 1978-1990, 1988  
 A:Title: Antifolate-resistant Chinese hamster cells. Molecular basis for the biochemical  
 lines.

A:Reference number: A28274; MUID:88115326; PMID:3339001  
 A:Accession: A28274  
 A:Molecule type: mRNA  
 A:Residues: 1-186 <MEL>  
 A:Cross-references: UNIPROT:Q5JH80  
 A:Experimental source: antifolate-resistant cell line DC-3P/A75  
 R:Mitchell, P.J.; Urlaub, G.; Chasin, L.  
 Mol. Cell. Biol. 6, 1926-1935, 1986  
 A:Title: Spontaneous splicing mutations at the dihydrofolate reductase locus in Chinese  
 hamster cells.  
 A:Reference number: I48104; MUID:87064481; PMID:3023911  
 A:Accession: I48104  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 88-160 <RES>  
 A:Cross-references: GB:M13477; NID:G191049; PIDN:AAA36973.1; PID:9553838  
 A:Comment: This enzyme catalyzes the NADPH-dependent reduction of 7,8-dihydrofolate to 5,  
 8-dihydrofolate.  
 C:Genetics:  
 A:Introns: 122/3  
 A:Note: the list of introns may be incomplete  
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology  
 C:Keywords: methotrexate resistance; NADP; oxidoreductase; trimethoprim resistance  
 F:3-125/Domain: type I dihydrofolate reductase homology <DPR>  
 F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 90.9%; Score 889; DB 1; Length 186;  
 Best Local Similarity 91.3%; Pred. No. 8.7e-71; Indels 0; Gaps 0;  
 Matches 168; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNGIGKNGDLPWPLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI 60  
 DB 1 VRLNCIVAVSQNGIGKNGDLPWPLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI 60  
 QY 61 PEKNRPLKGRINLVLSRELKEPQGAHFLSLDLDALKEPELANKVDWVWIVGGSSV 120

Db 61 PEKNRPLKGRINLVLSRELKEPQGAHFLAKSLDLDALKEPELANKVDWVWIVGGSSV 120  
 QY 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 180  
 Db 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 180  
 QY 181 VYEK 184  
 Db 181 VYEK 184

RESULT 3  
 S42445  
 A:Description: catalyzes the reduction of dihydrofolic acid to tetrahydrofolic acid with  
 A:Pathway: tetrahydrofolate synthesis  
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology  
 C:Species: Cricetus griseus (Chinese hamster)  
 C:Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_change 11-Jun-1999  
 C:Accession: S42445  
 R:Melera, P.W.; Davide, J.P.; Hession, C.A.; Scotto, K.W.  
 Mol. Cell. Biol. 4, 38-48, 1984  
 A:Title: Phenotypic expression in Escherichia coli and nucleotide sequence of two Chinese  
 hamster cell lines.  
 A:Reference number: S42445; MUID:84141864; PMID:6366511  
 A:Accession: S42445  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-187 <MEL>  
 A:Cross-references: EMBL:K01164; NID:G191053; PIDN:AAA36974.1; PID:9304503  
 A:Note: the authors translated the codon AAC for residue 49 as Asp, CAG for residue 108  
 as Ser  
 C:Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology  
 C:Keywords: NADP; oxidoreductase  
 F:4-126/Domain: type I dihydrofolate reductase homology <DPR>

Query Match 89.6%; Score 876; DB 2; Length 187;  
 Best Local Similarity 89.7%; Pred. No. 1.2e-69; Indels 0; Gaps 0;  
 Matches 165; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNGIGKNGDLPWPLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI 60  
 Db 2 VRLNCIVAVSQNGIGKNGDLPWPLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI 61  
 QY 61 PEKNRPLKGRINLVLSRELKEPQGAHFLSLDLDALKEPELANKVDWVWIVGGSSV 120  
 Db 62 PEKNRPLKGRINLVLSRELKEPQGAHFLAKSLDLDALKEPELANKVDWVWIVGGSSV 121  
 QY 121 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 180  
 Db 122 YKEAMNHGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPYGVLSVQVEKGIKYKFE 181  
 QY 181 VYEK 184  
 Db 182 VYEK 185

RESULT 4  
 RDMSD  
 A:Description: catalyzes the reduction of dihydrofolic acid to tetrahydrofolic acid with  
 A:Pathway: tetrahydrofolate synthesis  
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology  
 C:Species: Mus musculus (house mouse)  
 C:Date: 24-Apr-1984 #sequence\_revision 13-Mar-1997 #text\_change 16-Aug-2004  
 C:Accession: S13096; S13880; I48328; I49672; A92253; A90792; I49633; A21149; A90  
 R:McIvor, R.S.; Simonsen, C.C.  
 Nucleic Acids Res. 18, 7025-7032, 1990  
 A:Title: Isolation and characterization of a variant dihydrofolate reductase cDNA from  
 Chinese hamster ovary cells.  
 A:Reference number: S13096; MUID:91088280; PMID:2263462  
 A:Accession: S13096  
 A:Molecule type: mRNA  
 A:Residues: 1-187 <MEL>  
 A:Cross-references: UNIPROT:P00375; EMBL:X56066  
 A:Note: the authors did not translate the codon for residue 1  
 submitted to the EMBL Data Library, October 1990  
 A:Reference number: S13880  
 A:Accession: S13880  
 A:Molecule type: mRNA

A;Residues: 1-13,'D','15-187 <SIM>  
A;Cross-references: EMBL:X56066; NID:G50710; PIDN:CAA39544.1; PID:G50711  
J;Crouse, G.F.; Simonsen, C.C.; McSwan, R.N.; Schimke, R.T.  
J. Biol. Chem. 257, 7887-7897, 1982  
A;Title: Structure of amplified normal and variant dihydrofolate reductase genes in mouse  
A;Reference number: I48328; MUID:8213979; PMID:6282858  
A;Accession: 148328  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-28 <RES>  
A;Cross-references: EMBL:V00735; NID:G50701; PIDN:CAA24113.1; PID:G1619305  
R;McGrogan, M.; Simonsen, C.C.; Smouse, D.T.; Farnham, P.J.; Schimke, R.T.  
J. Biol. Chem. 260, 2307-2314, 1985  
A;Title: Heterogeneity at the 5' termini of mouse dihydrofolate reductase mRNAs: Evidence  
for alternative splicing  
A;Reference number: I49672; MUID:85130969; PMID:2982814  
A;Accession: 149672  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-3,'A','5-28 <RES>  
A;Cross-references: GB:M10071; NID:G193331; PIDN:AAA37637.1; PID:G553915  
R;Stone, D.; Paterson, S.J.; Raper, J.H.; Phillips, A.W.  
J. Biol. Chem. 254, 480-488, 1979  
A;Title: The amino acid sequence of dihydrofolate reductase from the mouse lymphoma L1210  
A;Reference number: A92253; MUID:79109591; PMID:762074  
A;Accession: A92253  
A;Molecule type: protein  
A;Residues: 2-31,'P','33-122,'EQ','125-127,'E','129-173,'D','175-187 <STO>  
A;Experimental source: Lymphoma L1210 cells  
R;Nunberg, J.H.; Kaufman, R.J.; Chang, A.C.Y.; Cohen, S.N.; Schimke, R.T.  
Cell 19, 355-364, 1980  
A;Title: Structure and genomic organization of the mouse dihydrofolate reductase gene.  
A;Reference number: A90792; MUID:80132485; PMID:6244105  
A;Accession: A90792  
A;Molecule type: mRNA  
A;Residues: 2-24;50-127;154-187 <NUN>  
A;Note: the authors translated the codon CAG for residue 169 as Gly  
R;Chang, A.C.Y.; Nunberg, J.; Kaufman, R.J.; Erlich, H.A.; Schimke, R.T.; Cohen, S.N.  
Nature 275, 617-624, 1978  
A;Title: Phenotypic expression in E.coli of a DNA sequence coding for mouse dihydrofolate  
reductase  
A;Reference number: I49632; MUID:79032141; PMID:360074  
A;Accession: I49632  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-24 <RES>  
A;Cross-references: GB:M10722; NID:G192946; PIDN:AAA37524.1; PID:G192949  
A;Accession: I49633  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 50-122,'E','124-127 <RE4>  
A;Cross-references: GB:M10811; NID:G192947; PIDN:AAA37525.1; PID:G192950  
R;Simonsen, C.C.; Levinson, A.D.  
Proc Natl. Acad. Sci. U.S.A. 80, 2495-2499, 1983  
A;Title: Isolation and expression of an altered mouse dihydrofolate reductase cDNA.  
A;Reference number: A21119; MUID:83195084; PMID:6573667  
A;Accession: A21119  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 2-22,'P','24-31,'P','33-187 <S12>  
A;Cross-references: GB:V00734; NID:G50699; PIDN:CAA24112.1; PID:G50700  
C;Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology  
C;Keywords: methotrexate resistance; NADP; one-carbon metabolism; oxidoreductase  
F;4-126/Domain: type I dihydrofolate reductase homology <DFR>  
F;31.35,65,71/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 89.5%; Score 875; DB 1; Length 187;  
Best Local Similarity 88.7%; Pred. No. 1,5e-69;  
Matches 165; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
QY 1 VGSNCIVAVSQNMGIKNGKNDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60  
DB 2 VRPLNCIVAVSQNMGIKNGKNDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 61  
QY 61 PEKNRPLKGRINLVLSRELKPPQGAHFLSRSLDALKLTEQPELANKYVDMWVIYVGGSSV 120

## RESULT 6

RDPGD

dihydrofolate reductase (EC 1.5.1.3) - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 28-Feb-1980 #sequence\_revision 28-Feb-1980 #text\_change 16-Aug-2004

C;Accession: AC0389

R;Smith, S.L.; Patrick, P.; Stone, D.; Phillips, A.W.; Burchall, J.J.

DB 62 PEKNRPLKGRINLVLSRELKPPQGAHFLAKSLDALKLTEQPELANKYVDMWVIYVGGSSV 121  
QY 121 YKEAMNHPGHLKLFVTRINQDPESTFFPEIDLEKYLPEYPGVLSVQVEEKGIKYKFE 180  
DB 122 YQEMNQPGHLKLFVTRINQDPESTFFPEIDLEKYLPEYPGVLSVQVEEKGIKYKFE 181  
QY 181 VYEKND 186  
DB 182 VYEKND 187

## RESULT 5

S42446

dihydrofolate reductase (EC 1.5.1.3) - Chinese hamster

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004

C;Accession: S42446; I48106

R;Meler, P.W.; Davide, J.P.; Hession, C.A.; Scotto, K.W.

Mol. Cell. Biol. 4, 38-48, 1984

A;Title: Phenotypic expression in Escherichia coli and nucleotide sequence of two Chinese

A;Reference number: S42445; MUID:84141864; PMID:6366511

A;Accession: S42446

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-187 &lt;WEL&gt;

A;Cross-references: UNIPROT:Q64742; EMBL:X01165; NID:G191058; PIDN:AAA36976.1; PID:G304

A;Note: the authors translated the codon AAC for residue 49 as Asp, CAG for residue 128

168 as Ser

R;Mitchell, P.J.; Carothers, A.M.; Han, J.H.; Harding, J.D.; Kas, E.; Venolia, L.; Chas

Mol. Cell. Biol. 6, 425-440, 1986

A;Title: Multiple transcription start sites, DNase I-hypersensitive sites, and an oppos

A;Reference number: I48106; MUID:87064325; PMID:3023846

A;Accession: I48106

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-45 &lt;MIT&gt;

A;Cross-references: GB:M13129; NID:G191060; PIDN:AAA51447.1; PID:G553839

C;Genetics:

A;Gene: DHFR

A;Introns: 29/2

C;Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology

C;Keywords: NADP; oxidoreductase

F;4-126/Domain: type I dihydrofolate reductase homology &lt;DFR&gt;

Query Match 89.5%; Score 875; DB 2; Length 187;

Best Local Similarity 89.7%; Pred. No. 1,5e-69;

Matches 165; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMGIKNGKNDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 60

DB 2 VRPLNCIVAVSQNMGIKNGKNDLPWPLRNEFRYFORMTTSSVEGKQNLVINGKKTWFSI 61

QY 61 PEKNRPLKGRINLVLSRELKPPQGAHFLSRSLDALKLTEQPELANKYVDMWVIYVGGSSV 120

DB 62 PEKNRPLKGRINLVLSRELKPPQGAHFLAKSLDALKLTEQPELANKYVDMWVIYVGGSSV 121

QY 121 YKEAMNHPGHLKLFVTRINQDPESTFFPEIDLEKYLPEYPGVLSVQVEEKGIKYKFE 180

DB 122 YQEMNQPGHLKLFVTRINQDPESTFFPEIDLEKYLPEYPRVLPEVQVEEKGIKYKFE 181

QY 181 VYEK 184

DB 182 VYEK 185

J. Biol. Chem. 254, 11475-11484, 1979  
 A:Title: Porcine liver dihydrofolate reductase. Purification, properties, and amino acid  
 A:Reference number: A00389; MUID:80049777; PMID:500653  
 A:Accession: A00389

A:Molecule type: protein

A:Residues: 1-186 <SMI>

A:Cross-references: UNIPROT:P00377

A:Experimental source: liver

A:Note: Cys-162 may be modified in approximately 30% of the molecules

C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology

C:Keywords: NADP; oxidoreductase

F:3-125/Domain: type I dihydrofolate reductase homology <DPR>

F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 88.1%; Score 862; DB 1; Length 186;

Best Local Similarity 88.2%; Pred. No. 2e-68;

Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60

DB 1 VRPLNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDALKLTQPELANKVDMVMVVGSSV 120

DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDALKLTQPELANKVDMVMVVGSSV 120

QY 121 YKEAMNHGHLKLFVTRIMQDFESTFPPEIDLEKYLKLLPYPGVLSVQBEKGIKYKFE 180

DB 121 YKEAMNHGHLKLFVTRIMQDFESTFPPEIDLEKYLKLLPYPGVLSVQBEKGIKYKFE 180

QY 181 VYEKN 186

DB 181 VYEKN 186

#### RESULT 7

ROBOD

dihydrofolate reductase (EC 1.5.1.3) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 15-Oct-1982 #sequence\_revision 15-Oct-1982 #text\_change 16-Aug-2004

A:Accession: A00388

A:Residues: 1-186 <LAI>

A:Experimental source: liver

C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology

C:Keywords: NADP; oxidoreductase

F:3-125/Domain: type I dihydrofolate reductase homology <DPR>

F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 87.1%; Score 852; DB 1; Length 186;

Best Local Similarity 86.0%; Pred. No. 1.5e-67;

Matches 160; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60

DB 1 VRPLNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDALKLTQPELANKVDMVMVVGSSV 120

DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDALKLTQPELANKVDMVMVVGSSV 120

QY 121 YKEAMNHGHLKLFVTRIMQDFESTFPPEIDLEKYLKLLPYPGVLSVQBEKGIKYKFE 180

DB 121 YKEAMNHGHLKLFVTRIMQDFESTFPPEIDLEKYLKLLPYPGVLSVQBEKGIKYKFE 180

QY 181 VYEKN 186

DB 181 VYEKN 186

DB 181 VYEKN 186

#### RESULT 8

RDBE11

dihydrofolate reductase (EC 1.5.1.3) - saimirine herpesvirus 1 (strain 11)

C:Species: saimirine herpesvirus 1

A:Note: host Saimiri sciureus (common squirrel monkey)

C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 16-Aug-2004

C:Accession: A29954; B36806

C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology

C:Keywords: NADP; oxidoreductase

F:3-125/Domain: type I dihydrofolate reductase homology <DPR>

F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 88.1%; Score 862; DB 1; Length 186;

Best Local Similarity 88.2%; Pred. No. 2e-68;

Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60

DB 1 VRPLNCIVAVSONMGIGKNGDLPWFLNRPYFQMTTSSVEGKQNLVIMGKKTWFSI 60

QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDALKLTQPELANKVDMVMVVGSSV 120

DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDALKLTQPELANKVDMVMVVGSSV 120

QY 121 YKEAMNHGHLKLFVTRIMQDFESTFPPEIDLEKYLKLLPYPGVLSVQBEKGIKYKFE 180

DB 121 YKEAMNHGHLKLFVTRIMQDFESTFPPEIDLEKYLKLLPYPGVLSVQBEKGIKYKFE 180

QY 181 VYEKN 186

DB 181 VYEKN 186

#### RESULT 9

S14840

dihydrofolate reductase (EC 1.5.1.3) - saimirine herpesvirus 1 (strain 484-77)

C:Species: saimirine herpesvirus 1

A:Variety: strain 484-77

C>Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 11-Jun-1999

C:Accession: S14840

R:Geck, P.; Whitaker, S.A.; Medveczky, M.M.; Last, T.J.; Medveczky, P.G.

submitted to the EMBL Data Library, March 1991

A:Description: Small RNAs expressed by a highly oncogenic strain of Herpesvirus saimirine

A:Reference number: S14840

A:Accession: S14840

A:Molecule type: DNA  
A:Residues: 1-186 <GEC>  
A:Cross-references: EMBL:X58774; NID:G60412; PIDN:CAA41575.1; PID:G60413  
A:Experimental source: strain 484-77  
C:Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology  
C:Keywords: NADP; oxidoreductase  
F:4-125/Domain: type I dihydrofolate reductase homology <DPR>  
F:31.35,64,70/Binding site: substrate (Asp, Phe, Asn, Arg) #status predicted

Query Match 79.0%; Score 772.5; DB 2; Length 186;  
Best Local Similarity 81.3%; Pred. No. 1.5e-60;  
Matches 148; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

QY 4 LNCIVAVQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSIPEK 63  
DB 5 LNCIVAVQNMIGKNGKGLPPLTNDPKYFQRM-TTSSVKNQNLVIMGKKTWFSIPEK 63

QY 64 NRPLKGRINLVLSRELKPPQGAHFLSRSLDALKLTEQPELANKVDVWVIVGSSVYKE 123  
DB 64 NRPLKDRINLVLSKLEIPIGHAFLARSLNDALKLTEQPELVNKNVDMVWVIVGSSVYKD 123

QY 124 AMNHGCHLKFVTRIMQFESDTPFPPEIDLEKYLPEYPGVLSDVQEEKGIKYKFEVYE 183  
DB 124 AMNYSGLHLKFVTRIMQFESDTPFPPEIDLEKYLPEYPGVLSDVQEEKGIKYKFEVYE 183

QY 184 KN 185  
DB 184 KN 185

RESULT 10  
ROBERS  
dihydrofolate reductase (EC 1.5.1.3) - saimirine herpesvirus 1 (strain 488)  
C:Species: saimirine herpesvirus 1  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 16-Aug-2004  
C:Accession: E34770  
R:Biesinger, B.; Trimble, J.J.; Desrosiers, R.C.; Fleckenstein, B.  
Virology 176, 505-514, 1990  
A:Title: The divergence between two oncogenic Herpesvirus saimiri strains in a genomic  
A:Reference number: A34770; MUID:90266466; PMID:2161148  
A:Accession: E34770  
A:Molecule type: DNA  
A:Residues: 1-213 <BIE>  
A:Cross-references: EMBL:M55264; NID:G331005; PIDN:AAA72932.1; PID:G331010  
C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology  
C:Keywords: methotrexate resistance; NADP; oxidoreductase; trimethoprim resistance  
F:4-125/Domain: type I dihydrofolate reductase homology <DPR>  
F:31.35,64,70/Binding site: substrate (Asp, Phe, Asn, Arg) #status predicted

Query Match 78.1%; Score 763.5; DB 1; Length 213;  
Best Local Similarity 81.2%; Pred. No. 1.1e-59;  
Matches 147; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

QY 4 LNCIVAVQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSIPEK 63  
DB 5 LNCIVAVQNMIGKNGKGLPPLTNDPKYFQRM-TTSSVKNQNLVIMGKKTWFSIPEK 63

QY 64 NRPLKGRINLVLSRELKPPQGAHFLSRSLDALKLTEQPELANKVDVWVIVGSSVYKE 123  
DB 64 NRPLKDRINLVLSKLEIPIGHAFLARSLNDALKLTEQPELVNKNVDMVWVIVGSSVYKD 123

QY 124 AMNHGCHLKFVTRIMQFESDTPFPPEIDLEKYLPEYPGVLSDVQEEKGIKYKFEVYE 183  
DB 124 AMNYSGLHLKFVTRIMQFESDTPFPPEIDLEKYLPEYPGVLSDVQEEKGIKYKFEVYE 183

QY 184 K 184  
DB 184 K 184

RESULT 11  
RDCHD  
dihydrofolate reductase (EC 1.5.1.3) - chicken

C:Species: Gallus gallus (chicken)  
C:Date: 31-Jul-1980 #sequence\_revision 31-Jul-1980 #text\_change 16-Aug-2004  
C:Accession: A00390; S65557  
R:Kumar, A.A.; Blankenship, D.T.; Kaufman, B.T.; Freisheim, J.H.  
Biochemistry 19, 667-678, 1980  
A:Title: Primary structure of chicken liver dihydrofolate reductase.  
A:Reference number: A00390; MUID:80130564; PMID:6766736  
A:Accession: A00390  
A:Molecule type: protein  
A:Residues: 1-189 <KUM>  
A:Cross-references: UNIPROT:P00378  
R:Pan, Y.; Ju, M.; Zhou, J.; Tsou, C.  
Biochem. J. 315, 97-102, 1996  
A:Title: Activation of chicken liver dihydrofolate reductase by urea and guanidine hydr  
A:Reference number: S65557; MUID:96207568; PMID:8670138  
A:Accession: S65557  
A:Molecule type: protein  
A:Residues: 19-22;138-140,'Q',158-161 <PAN>  
C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology  
C:Keywords: NADP; oxidoreductase  
F:3-123/Domain: type I dihydrofolate reductase homology <DPR>  
F:30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted

Query Match 74.6%; Score 730; DB 1; Length 189;  
Best Local Similarity 74.6%; Pred. No. 8e-57;  
Matches 138; Conservative 24; Mismatches 23; Indels 0; Gaps 0;

QY 1 VGSINCIIVAVSQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI 60  
DB 1 VRSLNSIVAVQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSI 60

QY 61 PEKNRPLKGRINLVLSRELKPPQGAHFLSRSLDALKLTEQPELANKVDVWVIVGSSV 120  
DB 61 PEKNRPLKDRINLVLSRELKPPQGAHFLSRSLDALKLTEQPELANKVDVWVIVGSSV 120

QY 121 YKAMNHGCHLKFVTRIMQFESDTPFPPEIDLEKYLPEYPGVLSDVQEEKGIKYKFE 180  
DB 121 YKAAEKPKNHRLFVTRILHEFESDTPFPPEIDLEKYLPEYPGVLSDVQEEKGIKYKFE 180

QY 181 VYEKN 185  
DB 181 VYOKS 185

RESULT 12  
S17984  
dihydrofolate reductase (EC 1.5.1.3) - forest day mosquito  
C:Species: Aedes albopictus (forest day mosquito)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S17984  
R:Shotkoski, F.A.; Fallon, A.M.  
Eur. J. Biochem. 201, 157-160, 1991  
A:Title: An amplified insect dihydrofolate reductase gene contains a single intron.  
A:Reference number: S17984; MUID:92007869; PMID:1915358  
A:Accession: S17984  
A:Molecule type: DNA  
A:Residues: 1-186 <SHO>  
A:Cross-references: UNIPROT:P28019; EMBL:X60192; NID:G5555; PIDN:CAA42748.1; PID:G5556  
C:Genetics:  
A:Introns: 27/2  
C:Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology  
C:Keywords: NADP; oxidoreductase  
F:3-123/Domain: type I dihydrofolate reductase homology <DPR>

Query Match 40.7%; Score 398.5; DB 2; Length 186;  
Best Local Similarity 44.5%; Pred. No. 9.7e-28;  
Matches 81; Conservative 36; Mismatches 56; Indels 9; Gaps 4;

QY 7 IVAVSQNMIGKNGDLPPFLRNEFRYFQMTTSSVEGKQNLVIMGKKTWFSIPEK 66  
DB 7 IVAVCANGGIGIKGDLPPFLR-LQELKYFGRMTKKIQDSGKRNAINGRKTYFGVPESKRP 65

QY 67 LKGRINLVLSRELKPPQGAH-----FLSRSLDALKLTEQPELANKVDVWVIVGSSVYK 122

Db 66 LPERLNIILTR--DPSANAYSEVWVCTSQEALKKLDEAPLVNENIENWIVGNNAVYK 122  
 QY 123 EAMNHPGHLKLVTRIMQDFSDTFFPIDLEKYKLLPEYFGVLSDVQEEKGIYKPEVY 182  
 Db 123 EAMQSDRCHRIYLTETFECDFAFPRTSD-FOLVAKDDVDVPEDIQEENGIOYQYRIY 181  
 QY 183 EK 184  
 Db 182 EK 183

RESULT 13  
 A:Species: Drosophila melanogaster  
 C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 16-Aug-2004  
 C:Accession: A53803  
 R:Haag, H.; Tyshenko, M.G.; Walker, V.K.  
 J. Biol. Chem. 269, 15179-15185, 1994  
 A:Title: Dihydrofolate reductase of Drosophila. Cloning and expression of a gene with a  
 A:Reference number: A53803; MUID:94253079; PMID:8195153  
 A:Accession: A53803  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-182 <HAO>  
 A:Cross-references: UNIPROT:P17719; GB:U06861; NID:G500629; PID:AA19051.1; PID:G500630  
 C:Genetics:  
 A:Gene: Dhfr  
 A:Cross-references: FlyBase:FBgn0004087  
 A:Introns: 27/2  
 C:Superfamily: Dihydrofolate reductase; type I dihydrofolate reductase homology  
 C:Keywords: NADP; oxidoreductase  
 F:3-122/Domain: type I dihydrofolate reductase homology <DFR>

Query Match 40.7%; Score 398; DB 2; Length 182;  
 Best Local Similarity 46.0%; Pred. No. 1e-27;  
 Matches 86; Conservative 37; Mismatches 48; Indels 16; Gaps 6;  
 QY 5 NCIVAVSONMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSIPEKN 64  
 Db 5 NLIVAVCNFGIGIRGDLFWP-IKSELKYFSRTTKRTSDPTKQNAVVMGRKTYEVPESK 63  
 QY 65 RLKGRINLVLSRELKEP--PGAHFLSRDLDALKLTOPELANKVDMVWIVGSSVYK 122  
 Db 64 RLPLRLNIVLSTLQESDLFAGV-LLCPNLETAKLLEE--QNEVENIWIIVGSGVYE 119  
 QY 123 EAMNHPGHLKLVTRIMQDFSDTFFPIDLEKYKLLPEYFGVLSDVQEEKGIYK 178  
 Db 120 EAMASPRCHRLVITQIMQKFCDDTFFPAIPDSFREAVPD----SDMPLGVQCEENGIKPE 174  
 QY 179 FEVYEKN 185  
 Db 175 YKILEKH 181

RESULT 14  
 A:Species: Homo sapiens (man)  
 C:Date: 02-Aug-1996 #sequence\_revision 31-Dec-1996 #text\_change 20-Apr-2000  
 C:Accession: I73445  
 R:Masters, J.N.; Yang, J.K.; Cellini, A.; Attardi, G.  
 C: Mol. Biol. 167, 23-36, 1993  
 A:Title: A human dihydrofolate reductase pseudogene and its relationship to the multiple  
 A:Reference number: 156377; MUID:83241747; PMID:6306253  
 A:Accession: I73445  
 A:Status: translated from GB/EMBL/DBJ; conceptual translation of pseudogene  
 A:Molecule type: mRNA  
 A:Residues: 1-97 <NAA>  
 A:Cross-references: GB:J00146; NID:g182732; PIDN:AAA52469.1; PID:G553296  
 C:Genetics:  
 A:Gene: GDB:DHFRP1

A:Cross-references: GDB:I19093  
 A:Map position: 18q12.1-18q12.1  
 C:Keywords: pseudogene

Query Match 36.6%; Score 358; DB 4; Length 97;  
 Best Local Similarity 78.7%; Pred. No. 1.5e-24;  
 Matches 70; Conservative 6; Mismatches 13; Indels 0; Gaps 0;  
 QY 1 VGSINCIVAVSONMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60  
 Db 2 VSLINCIVAVSONMGIGKNGDLPWPLRNEFRYFORVTTSSVEGKQNLVIMGKKTWFSI 61

QY 61 PEKNRELKGRINLVLSRELKEP--PGAHFL 89  
 Db 62 PEKNRELKGRINLVLRDRDHKNLHKEINF 90

RESULT 15  
 T19778  
 hypothetical protein C36B1.7 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: T19778  
 R:Lennard, N.  
 submitted to the EMBL Data Library, September 1996  
 A:Reference number: Z19176  
 A:Accession: T19778  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-189 <WIL>  
 A:Cross-references: UNIPROT:O93341; EMBL:Z80215; PIDN:CAB02272.1; GSPDB:GN00019; GESP:G3  
 A:Experimental source: clone C36B1  
 C:Genetics:  
 A:Gene: CESP:C36B1.7  
 A:Map position: 1  
 A:Introns: 45/3; 89/2; 140/2  
 C:Superfamily: type I dihydrofolate reductase; type I dihydrofolate reductase homology

Query Match 32.7%; Score 319.5; DB 2; Length 189;  
 Best Local Similarity 36.0%; Pred. No. 8.5e-21;  
 Matches 64; Conservative 41; Mismatches 70; Indels 3; Gaps 2;  
 QY 4 LNCIVAVSONMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSIPEK 63  
 Db 4 MLLIVAMDREGGIGKNGVLPWR-IKKDMQYFASVTKNVSDQSKRNVLMGRKWCESIPT 62  
 QY 64 NRPLKGRINLVLSRELKEP--PGAHFLSRDLDALKLTOPELANKVDMVWIVGSSVYK 123  
 Db 63 RRPLAGRLNIVLSRQLPAQKSDDYIVVNSLEAAMKLLSEPPFVDSIETIWNIGGAEIYDL 122  
 QY 124 AMNHPGHLKLVTRIMQDFSDTFFPIDLEKYKLL--PEYFGVLSDVQEEKGIYK 179  
 Db 123 ALRENLVDEIHTRIFKFEADVHLKSLDFSQKQVQNAEVSSENSEIFEENGLAFEP 180

Search completed: November 19, 2004, 13:52:42  
 Job time : 17 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 13:48:23 ; Search time 69 Seconds  
(without alignments)

1551.010 Million cell updates/sec

Title: US-10-650-417-7

Perfect score: 978

Sequence: 1 VGSUNCIIVASQNMIGKNG.....SDVQEEKGIKYKEVYEKND 186

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	968	99.0	186	1	DYR_HUMAN	P00374 homo sapien
2	968	99.0	187	2	AAH71996	Aah71996 homo sapi
3	965	98.7	187	2	Q6IRW8	Q6irw8 homo sapien
4	965	98.7	187	2	AAH70280	Aah70280 homo sapi
5	956	91.6	187	2	Q520D2	Q520d2 rattus norv
6	892	91.2	186	1	DYR_MESAU	P04753 mesocricetu
7	892	91.2	187	2	Q78EE3	Q78ee3 cricetus
8	887	90.7	187	2	Q78EH1	Q78eh1 cricetus
9	880	90.0	186	1	DYR_MOUSE	Bac27315 mus muscu
10	880	90.0	187	2	BAC27315	Bac27315 mus muscu
11	875	89.5	187	2	Q96XFO	Q96xf0 homo sapien
12	874	89.4	187	2	Q9P419	Q9p419 homo sapien
13	874	89.4	187	2	AAH63379	Aah63379 homo sapi
14	862	88.1	186	1	DYR_PIG	P00377 sus scrofa
15	852	87.1	186	1	DYR_BOVIN	P00376 bos taurus
16	907	82.5	187	1	DYR_SHV21	P09503 saimirine
17	772.5	79.0	186	1	DYR_SHV24	P27421 saimirine
18	765.5	78.4	194	2	Q9DS83	Q9ds83 saimirine
19	763.5	78.1	213	1	DYR_SHV2C	P22573 saimirine
20	763.5	78.1	213	2	Q778B2	Q778b2 saimirine
21	763.5	78.1	213	2	CAC84296	Cac84296 saimirin
22	730	74.6	189	1	DYR_CHICK	P00378 gallus gall
23	599.5	61.3	188	2	Q9WRU3	Q9wr3 macaca mula
24	599.5	61.3	188	2	Q92M7	Q9i2m7 macaca mula
25	596	60.9	190	2	Q6IQS4	Q6iqs4 brachydanio
26	596	60.9	190	2	AAH71330	Aah71330 brachydan
27	596	60.9	191	2	Q98TR9	Q98tr9 brachydanio
28	473.5	48.4	210	2	O40919	O40919 human herpe
29	472.5	48.3	210	2	P90486	P90486 human herpe
30	399	40.8	182	1	DYR_DROME	P17719 drosophila
31	398.5	40.7	186	1	DYR_AEDAL	P28019 aedes albop

## RESULT 1

ID	DYR_HUMAN	STANDARD;	PRT;	186 AA.
AC	P00374; Q14130;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Dihydrofolate reductase (EC 1.5.1.3).			
GN	Nome=DHFR;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84162075; PubMed=6323448;			
RX	Chen M.-J., Shimada T., Moulton A.D., Cline A., Humphries R.K.,			
RA	Maizel J., Nienhuis A.W.;			
RT	"The functional human dihydrofolate reductase gene.";			
RL	J. Biol. Chem. 259:3933-3943(1984).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83183667; PubMed=6687716;			
RA	Masters J.N., Attardi G.;			
RT	"The nucleotide sequence of the cDNA coding for the human dihydrofolic acid reductase.";			
RL	Gene 21:59-63(1983).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84267838; PubMed=6235374;			
RA	Yang J.K., Masters J.N., Attardi G.;			
RT	"Human dihydrofolate reductase gene organization. Extensive conservation of the G + C-rich 5' non-coding sequence and strong intron size divergence from homologous mammalian genes.";			
RL	J. Mol. Biol. 176:169-187(1984).			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RX	MEDLINE=22338257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Mueny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

## ALIGNMENTS

32	376	38.4	188	2	QBMTJ0	Q8mtj0 haematobia
33	369	37.7	185	1	DYR_HELVI	Q9u8b8 heliothis v
34	367.5	37.6	181	2	Q7Q5L5	Q7q0l5 anophelies g
35	358	36.6	97	2	Q6I9O8	Q6i9g8 homo sapien
36	347	35.5	73	2	O9JHB0	Q9jhb0 cricetus
37	327	33.4	264	2	Q8JKV3	Q8jkv3 heliothis z
38	324.5	33.2	182	2	Q6WEA6	Q6wea6 hartmannell
39	324.5	33.2	182	2	AAQ02617	Aaq02617 hartmanne
40	319.5	32.7	182	2	Q6WEA2	Q6wea2 hartmannell
41	319.5	32.7	182	2	Q6WEA8	Q6wea8 hartmannell
42	319.5	32.7	182	2	AAQ02615	Aaq02615 hartmanne
43	319.5	32.7	182	2	AAQ02621	Aaq02621 hartmanne
44	319.5	32.7	189	1	DYR_CAEEL	Q93341 caenorhabdi
45	317.5	32.5	182	2	Q6WEA4	Q6wea4 hartmannell

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallick D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE=88254806; PubMed=3383852;  
 RA Oefner C., D'Arcy A., Winkler F.K.,  
 RT "Crystal structure of human dihydrofolate reductase complexed with  
 RT folate.",  
 RL Eur. J. Biochem. 174:377-385 (1988).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 RX MEDLINE=91064350; PubMed=2248959;  
 RA Davies J.F., Delcamp T.J., Prendergast N.J., Ashford V.A.,  
 RA Freisheim J.H., Kraut J.,  
 RT "Crystal structures of recombinant human dihydrofolate reductase  
 RT complexed with folate and 5-deaza-folate.",  
 RL Biochemistry 29:9467-9479 (1990).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RX MEDLINE=98042281; PubMed=9374868;  
 RA Cody V., Galitsky N., Luft J.R., Pangborn W., Blakley R.L.,  
 RA Ganjee A.,  
 RT "Comparison of two independent crystal structures of human  
 RT dihydrofolate reductase ternary complexes reduced with nicotinamide  
 RT adenine dinucleotide phosphate and the very tight-binding inhibitor  
 RT PT523.",  
 RL Biochemistry 36:13897-13903 (1997).  
 RN [8]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=92118795; PubMed=1731871;  
 RA Stockman B.J., Nirmala N.R., Wagner G., Delcamp T.J., Deyarman M.T.,  
 RA Freisheim J.H.,  
 RT "Sequence-specific 1H and 15N resonance assignments for human  
 RT dihydrofolate reductase in solution.",  
 RL Biochemistry 31:218-229 (1992).  
 CC -1- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-  
 CC dihydrofolate + NADPH.  
 CC -1- PATHWAY: Essential step for de novo glycine and purine synthesis,  
 CC DNA precursor synthesis, and for the conversion of dUMP to dTMP.  
 CC -1- SIMILARITY: Belongs to the dihydrofolate reductase family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; J00140; AAA58485.1; -;  
 DR EMBL; V00507; CAA23765.1; -;  
 DR EMBL; J00139; AAA58484.1; -;  
 DR EMBL; X01612; AAA58484.1; JOINED.  
 DR EMBL; X01613; AAA58484.1; JOINED.  
 DR EMBL; J00138; AAA58484.1; JOINED.  
 DR EMBL; X01614; AAA58484.1; JOINED.  
 DR EMBL; X00855; CAA25409.1; -;  
 DR EMBL; X00856; CAA25409.1; JOINED.  
 DR EMBL; X00857; CAA25409.1; JOINED.  
 DR EMBL; X00858; CAA25409.1; JOINED.  
 DR EMBL; X00859; CAA25409.1; JOINED.  
 DR EMBL; BC000192; AAH00192.1; -;  
 DR EMBL; BC003584; AAH03584.2; -;  
 DR PIR; A22551; RDHUF.  
 DR PDB; 1B0CF; X-ray; A=1-186.  
 DR PDB; 1DHF; X-ray; A/B=1-186.  
 DR PDB; 1DLR; X-ray; @=1-186.  
 DR PDB; 1DLS; X-ray; @=1-186.  
 DR PDB; 1DRF; X-ray; @=1-186.  
 DR PDB; 1HFP; X-ray; @=1-186.

DR PDB; 1HFO; X-ray; @=1-186.  
 DR PDB; 1HFR; X-ray; @=1-186.  
 DR PDB; 1KMS; X-ray; A=1-186.  
 DR PDB; 1KVV; X-ray; A=1-186.  
 DR PDB; 1MVS; X-ray; A=1-186.  
 DR PDB; 1MVT; X-ray; A=1-186.  
 DR PDB; 1OHJ; X-ray; @=1-186.  
 DR PDB; 1OHK; X-ray; @=1-186.  
 DR PDB; 1PD8; X-ray; A=1-186.  
 DR PDB; 1PD9; X-ray; A=1-186.  
 DR PDB; 1PDB; X-ray; A=1-186.  
 DR PDB; 2DHF; X-ray; A/B=1-186.  
 DR HSC-2DPAGE; P00374; HUMAN.  
 DR Genew; HGNC:2861; DHFR.  
 DR MIM; 126060; -;  
 DR GO; GO:0004146; F: dihydrofolate reductase activity; NAS.  
 DR GO; GO:0006545; P: glycine biosynthesis; NAS.  
 DR GO; GO:0009165; P: nucleotide biosynthesis; NAS.  
 DR InterPro; IPR001796; DHFR.  
 DR Pfam; PF00186; Dihfolate\_red; 1.  
 DR PRINTS; PR00070; DHFR.  
 DR PROSITE; PS00075; DHFR; 1.  
 KW 3D-structure; NADP; One-carbon metabolism; Oxidoreductase.  
 FT INIT\_MET 0  
 FT STRAND 4 10  
 FT TURN 12 13  
 FT STRAND 15 18  
 FT TURN 19 20  
 FT STRAND 21 21  
 FT HELIX 28 39  
 FT TURN 44 45  
 FT STRAND 47 53  
 FT HELIX 54 59  
 FT HELIX 62 64  
 FT TURN 68 69  
 FT STRAND 71 75  
 FT TURN 84 85  
 FT STRAND 88 90  
 FT HELIX 93 100  
 FT TURN 101 101  
 FT TURN 103 108  
 FT STRAND 109 114  
 FT HELIX 118 125  
 FT TURN 126 126  
 FT STRAND 131 138  
 FT STRAND 146 147  
 FT TURN 153 155  
 FT STRAND 157 158  
 FT TURN 163 164  
 FT STRAND 170 172  
 FT TURN 173 174  
 FT STRAND 175 184  
 SQ SEQUENCE 186 AA; 21321 MW; EBB9E6A3ECA8CEDB CRC64;  
 Query Match 99.0%; Score 968; DB 1; Length 186;  
 Best Local Similarity 99.5%; Pred. No. 8.7e-78;  
 Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VGLNCIVAVSONMGIGKNGDLPPFLNERNRYFORMTTTSVECKQNLVIMGKKTWFSI 60  
 DB 1 VGLNCIVAVSONMGIGKNGDLPPFLNERNRYFORMTTTSVECKQNLVIMGKKTWFSI 60  
 QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQLANKVDMVWIVGSSV 120  
 DB 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQLANKVDMVWIVGSSV 120  
 QY 121 YKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQBEKGKIKYFE 180  
 DB 121 YKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSVQBEKGKIKYFE 180  
 QY 181 VYEKND 186  
 DB 181 VYEKND 186



## RESULT 2

AAH71996  
ID AAH71996 PRELIMINARY; PRT; 187 AA.  
AC AAH71996;  
DT 01-JUN-2004 (TREMELrel. 27, Created)  
DT 01-JUN-2004 (TREMELrel. 27, Last sequence update)  
DT 01-JUN-2004 (TREMELrel. 27, Last annotation update)  
DE Dihydrofolate reductase.  
GN DHFR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RA Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC071996; AAH71996.1; -  
SQ SEQUENCE 187 AA; 21453 MW; EBD3D1EC73E1566 CRC64;

Query Match 99.0%; Score 968; DB 2; Length 187;  
Best Local Similarity 99.5%; Pred. No. 8.7e-78;  
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60  
DB 2 VGLNCIVAVSQNMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 61  
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQPELANKVDWMTVVGSSV 120  
DB 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQPELANKVDWMTVVGSSV 121  
QY 121 YKEAMNHGPHGLKLFVTRIMQDFESDTFFPEIDLEKYLPEYGLSDVQEEKGIKYKFE 180  
DB 122 YKEAMNHGPHGLKLFVTRIMQDFESDTFFPEIDLEKYLPEYGLSDVQEEKGIKYKFE 181  
QY 181 VYEKND 186  
DB 182 VYEKND 187

## RESULT 3

Q61RW8  
ID Q61RW8 PRELIMINARY; PRT; 187 AA.  
AC Q61RW8;  
DT 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE Dihydrofolate reductase.  
GN DHFR;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pooled;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pooled;  
RA Strausberg R.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC070280; AAH70280.1; -  
DR InterPro; IPR001796; DHFR.  
DR Pfam; PF00186; DHFR\_1; 1.  
DR PRINTS; PR00070; DHFR.  
DR PROSITE; PS00075; DHFR; 1.  
SQ SEQUENCE 187 AA; 21467 MW; EBD21F03522FB94 CRC64;

Query Match 98.7%; Score 965; DB 2; Length 187;  
Best Local Similarity 98.9%; Pred. No. 1.6e-77;

Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 60  
DB 2 VGLNCIVAVSQNMGIGKNGDLPWPLRNEFRYFORMTTSSVEGKQNLVIMGKKTWFSI 61  
QY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQPELANKVDWMTVVGSSV 120  
DB 62 PEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDALKLTPQPELANKVDWMTVVGSSV 121  
QY 121 YKEAMNHGPHGLKLFVTRIMQDFESDTFFPEIDLEKYLPEYGLSDVQEEKGIKYKFE 180  
DB 122 YKEAMNHGPHGLKLFVTRIMQDFESDTFFPEIDLEKYLPEYGLSDVQEEKGIKYKFE 181  
QY 181 VYEKND 186  
DB 182 VYEKND 187

## RESULT 4

AAH70280  
ID AAH70280 PRELIMINARY; PRT; 187 AA.  
AC AAH70280;  
DT 01-JUN-2004 (TREMELrel. 27, Created)  
DT 01-JUN-2004 (TREMELrel. 27, Last sequence update)  
DT 01-JUN-2004 (TREMELrel. 27, Last annotation update)  
DE Hypothetical protein.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pooled;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pooled;  
 RX Strausberg R.;  
 RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC070280; AAH70280.1; --  
 KW Hypothetical protein.  
 SQ SEQUENCE 187 AA; 21467 MW; EBD21F03522FB94 CRC64;  
 Query Match 98.7%; Score 965; DB 2; Length 187;  
 Best Local Similarity 98.9%; Pred. No. 1.6e-77;  
 Matches 184; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VGLNCIVAVSQNMIGKNGDLPWPLRNEFRYQRMITTSVEGKQNLVIMGKKTWFSI 60  
 DB 1 VGLNCIVAVSQNMIGKNGDLPWPLRNEFRYQRMITTSVEGKQNLVIMGKKTWFSI 61  
 QY 61 PEKNRPLKGRINLVLSRELKPPQGAHFLSRSLDALKLTQPELANKVDMLVVGSSV 120  
 DB 62 PEKNRPLKGRINLVLSRELKPPQGAHFLSRSLDALKLTQPELANKVDMLVVGSSV 121  
 QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYLPPYPGVLSVDQBEKGIKYKFE 180  
 DB 122 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYLPPYPGVLSVDQBEKGIKYKFE 181  
 QY 181 VYEKND 186  
 DB 182 VYEKND 187  
 RESULT 5  
 Q920D2 PRELIMINARY; PRT; 187 AA.  
 AC Q920D2;  
 DT 01-DEC-2001 (TREMELrel. 19, Created)  
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
 DE Dihydrofolate reductase.  
 GN Name=Dhfr;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=21393659; PubMed=11502523;  
 RA Wang Y.; Bruenn J.A.; Queener S.F.; Cody V.;  
 RT "Isolation of rat dihydrofolate reductase gene and characterization of  
 RT recombinant enzyme.";  
 RL Antimicrob. Agents Chemother. 45:2517-2523(2001).  
 DR EMBL; AF318150; AAL11500.1; --  
 DR HSSP; P00374; 1KMS.  
 DR GO: GO:0004146; F.dihydrofolate reductase activity; IEA.  
 DR GO: GO:0006545; P.glycine biosynthesis; IEA.  
 DR GO: GO:0009163; P.nucleotide biosynthesis; IEA.  
 DR InterPro; IPR001796; DHFR.  
 DR Pfam; PF00186; DHFR\_1; 1.  
 DR PRINTS; PR00070; DHFR.  
 DR PROSITE; PS00075; DHFR; 1.  
 SQ SEQUENCE 187 AA; 21638 MW; FE1DB4F3515F9B26 CRC64;  
 Query Match 91.6%; Score 896; DB 2; Length 187;  
 Best Local Similarity 89.8%; Pred. No. 2.1e-71;  
 Matches 157; Conservative 12; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 VGLNCIVAVSQNMIGKNGDLPWPLRNEFRYQRMITTSVEGKQNLVIMGKKTWFSI 60  
 DB 2 VPLNCIVAVSQNMIGKNGDLPWPLRNEFRYQRMITTSVEGKQNLVIMGKKTWFSI 61  
 QY 61 PEKNRPLKGRINLVLSRELKPPQGAHFLSRSLDALKLTQPELANKVDMLVVGSSV 120  
 DB 62 PEKNRPLKGRINLVLSRELKPPQGAHFLSRSLDALKLTQPELANKVDMLVVGSSV 121  
 QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYLPPYPGVLSVDQBEKGIKYKFE 180  
 DB 122 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYLPPYPGVLSVDQBEKGIKYKFE 181  
 QY 181 VYEKND 186  
 DB 182 VYEKND 187  
 RESULT 6  
 D1R MESAU STANDARD; PRT; 186 AA.  
 AC P04753;  
 DT 13-AUG-1987 (rel. 05, Created)  
 DT 01-FEB-1996 (rel. 33, Last sequence update)  
 DT 05-JUL-2004 (rel. 44, Last annotation update)  
 DE Dihydrofolate reductase (EC 1.5.1.3).  
 GN Name=DHFR;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8115326; PubMed=3339001;  
 RA Melera P.W., Davide J.P., Oen H.;  
 RT "Antifolate-resistant Chinese hamster cells. Molecular basis for the  
 RT biochemical and structural heterogeneity among dihydrofolate  
 RT reductases produced by drug-sensitive and drug-resistant cell lines.";  
 RL J. Biol. Chem. 263:1978-1990(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung fibroblast;  
 RX MEDLINE=84141864; PubMed=6366511;  
 RA Melera P.W., Davide J.P., Hession C.A., Scotto K.W.;  
 RT "Phenotypic expression in Escherichia coli and nucleotide sequence of  
 RT two Chinese hamster lung cell cDNAs encoding different dihydrofolate  
 RT reductases.";  
 RL Mol. Cell. Biol. 4:38-48(1984).  
 RN [3]  
 RP ERRATUM.  
 RA Melera P.W., Davide J.P., Hession C.A., Scotto K.W.;  
 RL Mol. Cell. Biol. 4:1001-1001(1984).

CC -!- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-dihydrofolate + NADPH.

CC -!- PATHWAY: Essential step for de novo glycine and purine synthesis, DNA precursor synthesis, and for the conversion of dUMP to dTMP.

CC -!- POLYMORPHISM: The sequence shown is that of A3-35. The two clones A3-35 and MQ19-97 represent allelic forms. They differ in their drug sensitivities, possibly because of the difference at position 22.

CC -!- MISCELLANEOUS: Overexpression of the dihydrofolate gene (generally involving gene amplification) results in resistance to the antitumor antifolate drugs methotrexate (MTX) and methasquin.

CC -!- MISCELLANEOUS: Cell line DC-3F/A3 produces 90% of its dihydrofolate reductase in the 21x pi 6.5 form.

CC -!- MISCELLANEOUS: Cell line DC-3F/MQ19 produces 90% of its dihydrofolate reductase in the 20K pi 6.7 form (DHFR97).

CC -!- SIMILARITY: Belongs to the dihydrofolate reductase family.

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DR EMBL; X01164; AAA36974.1; -.

DR EMBL; X01165; AAA36976.1; -.

DR EMBL; M19869; AAA36970.1; -.

DR HSP; P00374; 1KWS.

DR InterPro; IPR001796; DHFR.

DR Pfam; PF00186; Dihfolate\_red; 1.

DR PRINTS; PRO00070; DHFR.

KW PROSITE; PS00075; DHFR; 1.

KW Method:reductase resistance; NADP; One-carbon metabolism; Oxidoreductase; Polymorphism.

FT INIT\_MET 0 0

FT SITE 7 9 INVOLVED IN MTX BINDING (BY SIMILARITY).

FT SITE 22 22 INVOLVED IN MTX BINDING (BY SIMILARITY).

FT SITE 30 31 INVOLVED IN MTX BINDING (BY SIMILARITY).

FT SITE 34 34 INVOLVED IN MTX BINDING (BY SIMILARITY).

FT SITE 36 36 INVOLVED IN MTX BINDING (BY SIMILARITY).

FT SITE 59 69 INVOLVED IN MTX BINDING (BY SIMILARITY).

FT SITE 115 115 INVOLVED IN MTX BINDING (BY SIMILARITY).

FT SITE 136 136 INVOLVED IN MTX BINDING (BY SIMILARITY).

FT SITE 22 22 F -> L (in MQ19-97).

FT VARIANT 95 95 D -> N (in MQ19-97).

FT VARIANT 95 95 D -> N (in MQ19-97).

SQ SEQUENCE 186 AA; 21529 MW; A9795E1A6DC51D4E CRC64;

Query Match 91.2%; Score 892; DB 1; Length 186;  
Best Local Similarity 91.3%; Pred. No. 4.8e-71;  
Matches 168; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPWPLRNEFRYFQRMTTSSVEGKQNLVIMGKKTWFSI 60  
Db 1 VRPLNCIVAVSQNMIGKNGDLPWPLRNEFRYFQRMTTSSVEGKQNLVIMGKKTWFSI 60

QY 61 PEKRNPLGRNLVLSRELKPPQGAHFLSLDDALKLTPPELANKVDMVWVGSSV 120  
Db 61 PEKRNPLGRNLVLSRELKPPQGAHFLSLDDALKLTPPELANKVDMVWVGSSV 120

QY 121 YKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPGVLSDVQEEKGIKYKFE 180  
Db 121 YKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPGVLSDVQEEKGIKYKFE 180

QY 181 VYEK 184  
Db 181 VYEK 184

RESULT 7  
Q78EE3 PRELIMINARY; PRT; 187 AA.  
AC Q78EE3

DT 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DE 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE Dihydrofolate reductase [EC 1.5.1.3].

OS Cricetus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.

OC NCBI\_TaxID=10031;

OX [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=90243717; PubMed=2335526;

RX Dicker A.P., Volkenandt M., Schweitzer B.I., Banerjee D., Bartino J.R.;

RA "Identification and characterization of a mutation in the dihydrofolate reductase gene from the methotrexate-resistant Chinese hamster ovary cell line Pro-3 MTX-R111.";

RL J. Biol. Chem. 265:8317-8321(1990).

DR EMBL; M37124; AAA36971.1; -.

DR GO; GO:0004146; F:dihydrofolate reductase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR InterPro; IPR001796; DHFR.

DR Pfam; PF00186; DHFR\_1; 1.

DR PRINTS; PRO00070; DHFR.

DR PROSITE; PS00075; DHFR; 1.

KW Oxidoreductase.

SQ SEQUENCE 187 AA; 21660 MW; A91F85A74658C6F3 CRC64;

Query Match 91.2%; Score 892; DB 2; Length 187;  
Best Local Similarity 91.3%; Pred. No. 4.8e-71;  
Matches 168; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 VGSNCIVAVSQNMIGKNGDLPWPLRNEFRYFQRMTTSSVEGKQNLVIMGKKTWFSI 60  
Db 2 VRPLNCIVAVSQNMIGKNGDLPWPLRNEFRYFQRMTTSSVEGKQNLVIMGKKTWFSI 61

QY 61 PEKRNPLGRNLVLSRELKPPQGAHFLSLDDALKLTPPELANKVDMVWVGSSV 120  
Db 62 PEKRNPLGRNLVLSRELKPPQGAHFLSLDDALKLTPPELANKVDMVWVGSSV 121

QY 121 YKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPGVLSDVQEEKGIKYKFE 180  
Db 122 YKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYLPPGVLSDVQEEKGIKYKFE 181

QY 181 VYEK 184  
Db 182 VYEK 185

## RESULT 8

Q78EH1 PRELIMINARY; PRT; 187 AA.

AC Q78EH1

DT 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DE Dihydrofolate reductase.

OS Cricetus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.

OC NCBI\_TaxID=10031;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Lung;

RA Yu M., Melena P.W.;

RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.

DR EMBL; L15311; AAA36972.1; -.

DR InterPro; IPR001796; DHFR.

DR Pfam; PF00186; DHFR\_1; 1.

DR PRINTS; PRO00070; DHFR.

DR PROSITE; PS00075; DHFR; 1.

SQ SEQUENCE 187 AA; 21659 MW; A71F65ADECS26659 CRC64;

Query Match 90.7%; Score 897; DB 2; Length 187;  
 Best Local Similarity 90.8%; Pred. No. 1.3e-70;  
 Matches 167; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

OY 1 VGSINCIIVAVSONMGIGKNGDLPPFLRNEFRYFORWTTSSVVGKQNLVIMGRKTFWSI 60  
 DB 2 VPLNCIIVAVSONMGIGKNGDFPPLRNEFRYFORWTTSSVVGKQNLVIMGRKTFWSI 61  
 OY 61 PEKNRPLKGRINLVLSRELKEPPQGAHFLSLDLALKLTPQBELAKVDMVMTVGGSSV 120  
 DB 62 PEKNRPLKDRINLVLSRELKEPPQGAHFLSLDLALKLTPQBELAKVDMVMTVGGSSV 121  
 OY 121 YKEAMNHQCHULKLVTRIMQFESDTPFPIDLEKYLIPYGVLSVDQEKGIKYKEE 180  
 DB 122 YKEAMNQCHULKLVTRIMQFESDTPFPIDLEKYLIPYGVLSVDQEKGIKYKEE 181  
 OY 181 VYEK 184  
 DB 182 VYEK 185

RESULT 9  
 DNR MOUSE  
 ID DNR MOUSE STANDARD; PRT; 186 AA.  
 AC PC0375; P79593; Q61485; Q61487; Q61579;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 03-JUL-2004 (Rel. 44, Last annotation update)  
 DE Dihydrofolate reductase (EC 1.5.1.3).  
 GN Name=Dhfr;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OG Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Lymphoma;  
 RX MEDLINE=79109591; PubMed=762074;  
 RA Stone D., Paterson S.J., Raper J.H., Phillips A.W.;  
 RT "The amino acid sequence of dihydrofolate reductase from the mouse  
 lymphoma L1210.";  
 RL J. Biol. Chem. 254:480-488(1979).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82213979; PubMed=6282858;  
 RA Grouse G.F., Simonsen C.C., McEwan R.N., Schimke R.T.;  
 RT "Structure of amplified normal and variant dihydrofolate reductase  
 genes in mouse sarcoma S180 cells";  
 RL J. Biol. Chem. 257:7887-7897(1982).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83195084; PubMed=6573667;  
 RA Simonsen C.C., Levinson A.D.;  
 RT "Isolation and expression of an altered mouse dihydrofolate reductase  
 cDNA.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2495-2499(1983).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91088280; PubMed=2263462;  
 RA McIvor R.S., Simonsen C.C.;  
 RT "Isolation and characterization of a variant dihydrofolate reductase  
 cDNA from methotrexate-resistant murine L5178Y cells.";  
 RL Nucleic Acids Res. 18:7025-7032(1990).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Bisak S.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP SEQUENCE OF 1-23; 49-126 AND 153-186 FROM N.A.  
 RX MEDLINE=80132485; PubMed=6244105;  
 RA Nunberg J.H., Kaufman R.J., Chang A.C.Y., Cohen S.N., Schimke R.T.;  
 RT "Structure and genomic organization of the mouse dihydrofolate  
 reductase gene.";  
 RL Cell 19:355-364(1980).  
 RN [7]  
 RP SEQUENCE OF 1-23 AND 49-126 FROM N.A.  
 RX MEDLINE=79032141; PubMed=360074;  
 RA Chang A.C.Y., Nunberg J.H., Kaufman R.J., Erlich H.A., Schimke R.T.,  
 Cohen S.N.;  
 RT "Phenotypic expression in E. coli of a DNA sequence coding for mouse  
 dihydrofolate reductase.";  
 RL Nature 275:617-624(1978).  
 RN [8]  
 RP SEQUENCE OF 162-186 FROM N.A.  
 RX MEDLINE=82167639; PubMed=6121807;  
 RA Setzer D.R., McGrogan M., Schimke R.T.;  
 RT "Nucleotide sequence surrounding multiple polyadenylation sites in the  
 mouse dihydrofolate reductase gene.";  
 RL J. Biol. Chem. 257:5143-5147(1982).  
 RN [9]  
 RP SEQUENCE OF 1-27 FROM N.A.  
 RX MEDLINE=85130969; PubMed=2982814;  
 RA McGrogan M., Simonsen C.C., Smouse D.T., Farnham P.J., Schimke R.T.;  
 RT "Heterogeneity at the 5' termini of mouse dihydrofolate reductase  
 mRNAs. Evidence for multiple promoter regions.";  
 RL J. Biol. Chem. 260:2307-2314(1985).  
 CC -1- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-  
 dihydrofolate + NADPH.  
 CC -1- PATHWAY: Essential step for de novo glycine and purine synthesis,  
 DNA precursor synthesis, and for the conversion of dUMP to dTMP.  
 CC -1- SIMILARITY: Belongs to the dihydrofolate reductase family.  
 CC -----  
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 CC -----  
 CC EMBL; L26316; AAA37523.1; -  
 CC EMBL; J00387; AAA37638.1; -  
 CC EMBL; J00382; AAA37638.1; JOINED.  
 CC EMBL; J00383; AAA37638.1; JOINED.  
 CC EMBL; J00384; AAA37638.1; JOINED.  
 CC EMBL; J00385; AAA37638.1; JOINED.  
 CC EMBL; J00386; AAA37638.1; JOINED.  
 CC EMBL; V00731; CAB43539.1; -  
 CC EMBL; V00734; CAB43539.1; -  
 CC EMBL; BC005796; AAH05796.1; -  
 CC EMBL; M10722; AAA37524.1; -  
 CC EMBL; M10811; AAA37525.1; -  
 CC EMBL; V00733; CAB43544.1; -  
 CC EMBL; X56066; AAA39544.1; -  
 CC EMBL; M10071; AAA37637.1; -

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DR PIR; S13096; RDMSD.
DR HSP; P00374; IONS.
DR MGD; MG1:94890; Dhfr.
DR InterPro; IPR001796; DHFR.
DR Pfam; PF00186; Dihydrofolate_red; 1.
DR PRINTS; PR00070; DHFR.
DR PROSITE; PS00075; DHFR; 1.
KW Direct protein sequencing; NADP; One-carbon metabolism;
KW Oxidoreductase.
FT INIT MET 0
FT VARIANT 22 22
FT VARIANT 31 31
FT CONFLICT 3 3
FT CONFLICT 13 13
FT CONFLICT 122 122
FT CONFLICT 123 123
FT CONFLICT 127 127
FT CONFLICT 173 173
SQ SEQUENCE 186 AA; 21475 MW; 47C82AE2AC0DCA21 CRC64;
Query Match 90.0%; Score 880; DB 1; Length 186;
Best Local Similarity 89.2%; Pred. No. 5.6e-70;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGSNLCIVAVSONMGIGKNGDLPWPLRNEFRYQFMTTSSVEGKQNLVIMGKKTWFSI 60
DB 1 VRPLNCIVAVSONMGIGKNGDLPWPLRNEFRYQFMTTSSVEGKQNLVIMGKKTWFSI 60
QY 61 PEKNRPLKGRINLVLSRELKEPPGQAHFLSLRSLDALKLTPQELANKVDMVWIVGSSV 120
DB 61 PEKNRPLKDRINIVLSRELKEPPGQAHFLSLRSLDALKLTPQELANKVDMVWIVGSSV 120
QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYLLPEYGVLSVQVEKGKIKYKFE 180
DB 121 YQEAANNQPGHLKLVTRIMQDFESDTFFPEIDLGKYLPEYGVLSVQVEKGKIKYKFE 180
QY 181 VYEKND 186
DB 181 VYEKND 186
RESULT 10
BAC27315 PRELIMINARY; PRT; 187 AA.
AC BAC27315;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DE 13 days embryo forelimb cDNA, RIKEN full-length enriched library,
DE clone:5930436E06 product:DIHYDROFOLATE REDUCTASE, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.
OX NCBI_taxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
```

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[3]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Forelimb;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Forelimb;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK031241; BAC27315.1;
SQ SEQUENCE 187 AA; 21606 MW; 47AEF15F879B119C CRC64;
Query Match 90.0%; Score 880; DB 2; Length 187;
Best Local Similarity 89.2%; Pred. No. 5.6e-70;
Matches 166; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 VGSNLCIVAVSONMGIGKNGDLPWPLRNEFRYQFMTTSSVEGKQNLVIMGKKTWFSI 60
DB 2 VRPLNCIVAVSONMGIGKNGDLPWPLRNEFRYQFMTTSSVEGKQNLVIMGKKTWFSI 61
QY 61 PEKNRPLKGRINLVLSRELKEPPGQAHFLSLRSLDALKLTPQELANKVDMVWIVGSSV 120
DB 62 PEKNRPLKDRINIVLSRELKEPPGQAHFLSLRSLDALKLTPQELANKVDMVWIVGSSV 121
QY 121 YKEAMNHPGHLKLVTRIMQDFESDTFFPEIDLEKYLLPEYGVLSVQVEKGKIKYKFE 180
DB 122 YQEAANNQPGHLKLVTRIMQDFESDTFFPEIDLGKYLPEYGVLSVQVEKGKIKYKFE 181
QY 181 VYEKND 186
DB 182 VYEKND 187
RESULT 11
Q86XF0 PRELIMINARY; PRT; 187 AA.
ID Q86XF0
AC Q86XF0;
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DT 01-JUN-2003 (TREMELrel. 24, Created)  
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Hypothetical protein LOC200895.  
 GN Name=LOC200895;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC045541; AAH45541.1; -;  
 DR HSSP; P00374; 1KNS.  
 DR GO; GO:0004146; P:dihydrofolate reductase activity; IEA.  
 DR GO; GO:0006545; P:glycine biosynthesis; IEA.  
 DR GO; GO:0009165; P:nucleotide biosynthesis; IEA.  
 DR InterPro; IPR001796; DHER.  
 DR Pfam; PF00186; DHER\_1; 1.  
 DR PRINTS; PR00070; DHER.  
 KW Hypothetical protein.  
 SQ SEQUENCE 187 AA; 21620 MW; BA6548FB0F576FF7 CRC64;  
 Query Match 89.5%; Score 875; DB 2; Length 187;  
 Best Local Similarity 92.9%; Pred. No. 1.6e-69;  
 Matches 170; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
 QY 4 LNCIVAVSQNMIGKNGDLPMPFFLRNFRYQRMFTTSSVEGKONLVIMGKTFWFSIPEK 63  
 DB 5 LNCIVAVSQNMIGKNGDLPMPFFLRNFRYQRMFTTSSVEGKONLVIMGKTFWFSIPEK 64  
 QY 64 NRPLKGRNLVLSRELKEPPGGAHFLSDDALKLTPQELANKVDMWIVGSSVYKE 123  
 DB 65 NRPLKDRNLVLSRELKEPPGGAHFLSDDALKLTPQELANKVDMWIVGSSVYKE 124  
 QY 124 AMNHGHLKLVTRIMQDFSDTFFPBIIDLEKYLPEYFGVLSDVQEGKIKYKFEVE 183  
 DB 125 AMNHGHLKLVTRIMQDFSDTFFPBIIDLEKYLPEYFGVLSDVQEGKIKYKFEVE 184  
 QY 184 KND 186  
 DB 185 KOD 187  
 RESULT 12  
 Q6P419 PRELIMINARY; PRT; 187 AA.  
 DE Q6P419

AC Q6P419;  
 DT 05-JUL-2004 (TREMELrel. 27, Created)  
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
 DE LOC200895 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC063379; AAH63379.1; -;  
 DR InterPro; IPR001796; DHER.  
 DR Pfam; PF00186; DHER\_1; 1.  
 DR PRINTS; PR00070; DHER.  
 SQ SEQUENCE 187 AA; 21634 MW; BA6548FB0F410327 CRC64;  
 Query Match 89.4%; Score 874; DB 2; Length 187;  
 Best Local Similarity 92.3%; Pred. No. 1.9e-69;  
 Matches 169; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 4 LNCIVAVSQNMIGKNGDLPMPFFLRNFRYQRMFTTSSVEGKONLVIMGKTFWFSIPEK 63  
 DB 5 LNCIVAVSQNMIGKNGDLPMPFFLRNFRYQRMFTTSSVEGKONLVIMGKTFWFSIPEK 64  
 QY 64 NRPLKGRNLVLSRELKEPPGGAHFLSDDALKLTPQELANKVDMWIVGSSVYKE 123  
 DB 65 NRPLKDRNLVLSRELKEPPGGAHFLSDDALKLTPQELANKVDMWIVGSSVYKE 124  
 QY 124 AMNHGHLKLVTRIMQDFSDTFFPBIIDLEKYLPEYFGVLSDVQEGKIKYKFEVE 183  
 DB 125 AMNHGHLKLVTRIMQDFSDTFFPBIIDLEKYLPEYFGVLSDVQEGKIKYKFEVE 184  
 QY 184 KND 186  
 DB 185 KOD 187  
 RESULT 13  
 AAH63379 PRELIMINARY; PRT; 187 AA.  
 AC AAH63379  
 DT 02-MAR-2004 (TREMELrel. 27, Created)  
 DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)  
 DE LOC200895 protein.

OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;	
OX	[1]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Muscle;
RC	MEDLINE=2388257; PubMed=12477932;
RA	Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schestz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prance C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Cunnatne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Grinchew J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Townwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Muscle;
RA	Strausberg R.;
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC063379; AAH63379.1; -
SR	SEQUENCE 187 AA; 21634 MW; BA6548F80F410327 CRC64;
DQ	

Query Match	89.4%;	Score	874;	DB	2;	Length	187;
Best Local Similarity	92.3%;	Pred.	No. 1.9e-69;				
Matches	169;	Conservative	6;	Mismatches	8;	Indels	0;
Gaps	0;						
QY	4	LNCIVAVSQNMGI	GKNGDL	PWPF	LNRNFR	FRFQ	MTTSTSSVEGKONLIVIMGKRTWFSIPEK 63
DB	5	LNCIVAVSQNMGI	GKNGDL	PRPP	LNRNFR	FRFQ	MTTSTSSVEGKONLIVIMGRTWFSIPEK 64
QY	64	NRPLKGRINL	VL	SREL	KEPP	CGAHL	LSRLDDALKL
DB	65	NRPLKDRINL	VL	SREL	KEPP	CGAHL	LSRLDDALKL
QY	124	AMNHGHLK	LFVTR	IQMD	FESD	TFP	FI
DB	125	AMNHGHLK	LFVTR	IQMD	FESD	TFP	FI
QY	184	KND	186				
DB	185	KDD	187				

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RESULT 14
DYN_PIG
ID_DYN_PIG          STANDARD;          PRT;          186 AA.
AC      P00377;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Dihydrofolate reductase (EC 1.5.1.3).
GN      Name=DHFR;
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Liver;

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<p> RX MEDLINE=80049777; PubMed=500653;  RA Smith S.B., Patrick P., Stone D., Phillips A.W., Burchall J.J.;  RT "Porcine liver dihydrofolate reductase. Purification, properties, and  RL amino acid sequence.";  RJ J. Biol. Chem. 254:11475-11484(1979).  CC -1- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-  CC dihydrofolate + NADPH.  CC -1- PATHWAY: Essential step for de novo glycine and purine synthesis,  CC DNA precursor synthesis, and for the conversion of dUMP to dTMP.  CC -1- SIMILARITY: Belongs to the dihydrofolate reductase family.  DR PIR; A00389; RDPGD.  DR HSSP; P00374; 1KMS.  DR InterPro; IPR001796; DHFR.  DR Pfam; PF00186; Dihfolate_red; 1.  DR PRINTS; PR00070; DHFR.  DR PROSITE; PS00075; DHFR; 1.  KW Direct protein sequencing; NADP; One-carbon metabolism;  KW Oxidoreductase.  KW MOD RES 162 162 Cysteine derivative (partial).  FT MOD RES 162 162  SQ SEQUENCE 186 AA; 21455 MW; D05DB526FE5C13CE CRC64; </p>	<p> Query Match 88.1%; Score 862; DB 1; Length 186;  Best Local Similarity 88.2%; Pred. No. 2.2e-68;  Matches 164; Conservative 12; Mismatches 10; Indels 0; Gaps 0; </p>	<p> QY 1 VGSINCIIVASQNGKIGKNGDLWPPLRNEFRYFQRMITTSVEGKQNLVIMGKKTWFSI 60  DB 1 VRPLNCIVASQNGKIGKNGDLWPPLRNEYKYFQRMITTSVEGKQNLVIMGKKTWFSI 60  QY 61 PEKNRPLKGRINVLVSRLEKEPPQGAHFLRSISLDDALKLTQPELANKVDMMVIVGSSV 120  DB 61 PEKNRPLKGRINVLVSRLEKEPPQGAHFLAKSLDDALKLTQPELANKVDMMVIVGSSV 120  QY 121 YKEAMNHGHLKLFVIRIVQDPSDFTFPPIDILEKYKLLPEYGVLSDDVQBEKGIKYKFE 180  DB 121 YKEAMNHGHLRILVIRIVQDPSDFTFPPIDILEKYKLLSECVSPSDVQBEKGIKYKFE 180  QY 181 VYEKND 186  DB 181 VYEKN 186 </p>	<p> RESULT 15  DYN_BOVIN STANDARD; PRT; 186 AA.  ID ID DYN_BOVIN STANDARD; PRT; 186 AA.  AC AC P00376;  DT 21-JUL-1986 (Rel. 01, Created)  DT 21-JUL-1986 (Rel. 01, Last sequence update)  DT 05-JUL-2004 (Rel. 44, Last annotation update)  DE Dihydrofolate reductase (EC 1.5.1.3).  GN Name=DHFR;  OS Bos taurus (Bovine).  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  OC Bovinae; Bos  OC NCBI_TaxID=9913;  RN [1]  RP SEQUENCE.  RC TISSUE=Liver;  RX MEDLINE=83000246; PubMed=7115669;  RA Lai P.-H., Pan Y.-C.E., Gleisner J.M., Peterson D.L., Williams K.R.,  RA Blakley R.L.;  RT "Structure of dihydrofolate reductase: primary sequence of the bovine  RT liver enzyme.";  RL Biochemistry 21:3284-3294(1982).  CC -1- CATALYTIC ACTIVITY: 5,6,7,8-tetrahydrofolate + NADP(+) = 7,8-  CC dihydrofolate + NADPH.  CC -1- PATHWAY: Essential step for de novo glycine and purine synthesis,  CC DNA precursor synthesis, and for the conversion of dUMP to dTMP.  CC -1- SIMILARITY: Belongs to the dihydrofolate reductase family.  DR PIR; A00388; RDBOD.  DR HSSP; P00374; 1DHF.  DR InterPro; IPR001796; DHFR. </p>
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DR PFam; PF00186; Dihfolate_red; 1.
DR PRINTS; PR00070; DHER.
DR PROSITE; PS00075; DHER; 1.
KW Direct protein sequencing; NADP; One-carbon metabolism;
KW Oxidoreductase.
SQ SEQUENCE 186 AA; 21472 MW; A615136C7706677F CRC64;

Query Match      87.1%; Score 852; DB 1; Length 186;
Best Local Similarity 86.0%; Pred. No. 1.7e-67;
Matches 160; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 VGLNCIVAVSQNMGIGKNGDLPWFFLNFRYFQRMVTTSSVEGKQNLVIMGKKTWFSI 60
DB 1 VRPLNCIVAVSQNMGIGKNGDLPWFFLNFRYFQRMVTTSSVEGKQNLVIMGKKTWFSI 60
QY 61 PEKNRPLKGRINLVLSRELKEPPGCAHFLSRSLDDALKLREQPELANKVDVWVIWVGSSV 120
DB 61 PEKNRPLKDRINLVLSRELKEPPGCAHFLSRSLDDALKLREQPELANKVDVWVIWVGSSV 120
QY 121 YKEAMNHPGHLKLFVTRIMQDFESTPPPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKPE 180
DB 121 YKEAMNKGHVRLFVTRIMQDFESDAFPPEIDFEKYKLLPEYPGVPLDVQEEKGIKYKPE 180
QY 181 VYEKND 186
DB 181 VYEKNN 186

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Search completed: November 19, 2004, 13:49:40  
Job time : 71 secs